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ALIGNMENTS

AAW23979 standard; peptide; 5 AA. AAW23979; AAW23979 

Cadherin-mediated cell adhesion modulating peptide 1. (first entry) 23-JUL-1998

Cadherin-mediated; cell adhesion; drug delivery; treatment; cancer; angiogenesis; skin grafting; neurite growth; veterinary medicine; wound healing; tumour; metastasis carcinoma; leukaemia; modulation; organ transplant; neurological disease.

Synthetic.

note= "optional N-terminal acetylation" /note= "optional C-terminal amidation" Location/Qualifiers Modified-site Modified-site

WO9802452-A2

11-JUL-1997;

97WO-CA000489

96US-0021612P 12-JUL-1996;

(UYMC-) UNIV MCGILL.

Gour BJ; Blaschuk OW,

WPI; 1998-110522/10.

Cyclic peptide(s) that modulate cadherin-mediated cell adhesion - used to improve drug delivery through skin, to the brain etc., for treatment of cancer, angiogenesis etc., and to improve grafting of foreign tissue or neurite

Claim 8; Page 97; 133pp; English.

This is a cyclisised peptide capable of modulating cadherin-mediated cell adhesion. Cadherin-expressing cells can be detected from their reaction with the antibody that binds the peptides of the invention. These mediated by E., N., P. or R-cadherins (or other cadherins that include the amino acids HAV recognition sequence), specifically where these are twyressed by epithelial, endothelial, neural or tumour cells or ymphocytes. The peptides which inhibit cell adhesion are used to improve close stream), to tumours (particularly ovarian or bladder tumours or malanoma) and to the brain. They are also used to treat cancer (carcinoma, leukaemia or melanoma), inhibit metastasis and also inhibit malanoma, leukaemia or melanoma), inhibit metastasis and also inhibit congiagenesis in The peptides that stimulate adhesion are used to improve wound healing to promote adherence of foreign tissues (skin grafts or organ transplants), and to improve adherence to tissue culture surfaces and bloreactors. Other uses of the peptides are to induce apoptosis in cadherin-expressing cells, increase or decrease neurite outgrowth, to treat spinal cord injuries and de-myelising neurological diseases (specifically multiple sclerosis). They can be used for modulating the immune system (e.g. in cases of diabetes or rheumacoid arthritis) for preventing pregnancy and to increase vaso-permeability. The antibodies which bind to these peptides are also used to modulate cell adhesion and

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when coupled to a drug, to target the drug to cadherin-expressing cells. Diagnostic agents may also be delivered using the peptides in a skin patch, particularly where the agent generates a colour in contact with, e.g. cocanine, human immunodeficiency viral proteins, glucose or prostate specific antigen, particularly for home-testing kits. The peptides make it possible to deliver a wide range of drugs through the skin, avoiding parenteral administration, by-passing the gastro- intestinal system and
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ive 0; Mismatches 0;
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Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion; cadherin-mediated function; demyelinating neurological disease; multiple sclerosis; drug delivery; cancer; angiogenesis; immune system; central nervous system; apoptosis induction; cadherin-expression cell; pregnancy prevention; vasopermeability; synaptic stability; diabetes; rheumatoid arthritic; allergic response; learning; memory; antibody-mediated graft rejection; cyclic. Peptide inhibiting interaction of alpha-catenin and beta-catenin.

(first entry)

24-MAR-1999

Synthetic.

WO9845319-A2

15-OCT-1998

98WO-CA000322. 14-APR-1998; 97US-0043361P. 10-APR-1997;

(UYMC-) UNIV MCGILL.

Gour BJ; Blaschuk OW, WPI; 1999-024009/02.

New catenin modulating agents - comprising peptides having a sequence HAV or analogues or antibodies, used for modulating cadherin-mediated Eunctions

Claim 12; Page 78; 106pp; English.

The present sequence represents a peptide which is capable of inhibiting an interaction between alpha-catenin and beta-catenin. The peptide is used in modulating agents that are used for modulating cadherin-mediated functions. They can be used for disrupting interaction between alphacatenin and beta-catenin in a cell, inhibiting cell adhesion, e.g. between epithelial cells, endothelial cells, neural cells, tumour cells and lymphocytes, for treating a demyelinating neurological disease, e.g. multiple solerosis, for reducing unwanted cellular adhesion in a mammal, for enhancing the delivery of a drug through the skin of a mammal, for enhancing the delivery of a drug through in a mammal, for treating cancer in a mammal, for inhibiting angiogenesis in a mammal, for enhancing drug delivery to the central nervous system of a mammal, for inducing apoptosis in a cadherin-expression cell, for modulating the

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The present sequence represents a peptide which is capable of inhibiting an interaction between alpha-catenin and beta-catenin. The peptide is used in modulating agents that are used for modulating cablerin-mediated functions. They can be used for disrupting interaction between alphacatenin and beta-catenin in a cell, inhibiting cell adhesion, e.g. between eptthelial cells, endothelial cells, neural cells, tumour cells and lymphocytes, for treating a demyelinating neurological disease, e.g. multiple sclerosis, for reading unwanted cellular adhesion in a mammal, for enhancing the delivery of a drug through the skin of a mammal, for cancer in a mammal, for inhibiting angiogenesis in a mammal, for cancer in a mammal, for inhibiting angiogenesis in a mammal, for inducing apoptosis in a cadherin-expression cell, for modulating the immune system of a mammal, for preventing pregnancy in a mammal, for increasing vasopermeability in a mammal, or for inhibiting synaptic stability in a mammal. In particular they can be used for treating
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immune system of a mammal, for preventing pregnancy in a mammal, for increasing vasopermeability in a mammal, or for inhibiting synaptic stability in a mammal. In particular they can be used for treating diabetes, rheumatoid arthritic, allergic responses, antibody-mediated graft rejection or for stimulating learning and memory
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diabetes, rheumatoid arthritic, allergic responses, antibody-mediated
graft rejection or for stimulating learning and memory
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                                                                                  100.0%; Score 34; DB 2; Length 5; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                  Cadherin-mediated adhesion modulating cyclic peptide.
                                                                                                                                                                                                                                                                             AAY17108 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                    Stimulating beta-catenin mediated gene expression, cellular differentiation and hair growth, involves contacting cells with modulating agent capable of inhibiting interaction between alpha and beta
                                                                                                                             Beta-catenin; cadherin-mediated intercellular adhesion; cell differentiation; modulating agent; hair loss; skin exfoliation; internalisation moiety; flanking sequence; transcription; hearing loss.
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                                                                                                          Beta-catenin derived linear peptide SEQ ID NO: 22.
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                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 77pp; English
                                        AAB27334 standard; peptide; 5 AA.
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of free beta-catenin in the cell, and methods of stimulating the expression of genes involved in cellular differentiation, the transcription of which is under the control of beta-catenin. The peptides given in AAB27053-B27089, AAB27284-B27300 and AAB2730-B27351 can be used as modulating agents which interrupt the interaction between alpha and beta catenin, causing increased levels of the latter and stimulating the activation of beta-catenin mediated transcription. This can be used to stimulate cell differentiation, which can then be used to promote hair aprovement of photodamaged skin and to minimise wrinkles. The modulating peptide can also be used to reduce hearing loss resulting from inner ear disorders such as hyperacusis and tinnitus
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Beta-catenin, cadherin-mediated intercellular adhesion, cell differentiation, modulating agent, hair loss, skin exfoliation, internalisation moiety, flanking sequence, transcription, hearing loss,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:296.
                                                                                                                                                                                                                                                                                                                                                                                    /note= "the disulfide bond cyclises the molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 7; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY73790 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00265107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2000; 2000WO-CA000222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gour BJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-594308/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
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imidazole compounds of specified formulae that are peptidomimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting anglogenesis, enhancing development of cancer, the control mediating modulating the immune system, increasing vasopermeability, treating demyelinating the immune system, increasing vasopermeability, expressing cell on astrocytes, inhibiting angration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating neutre outgrowth, and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Linked to residue 5 to form a cyclic peptide, N-terminal acetyl or N-terminal CH3-502 group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to cell adhesion modulating agents that comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell adhesion modulating agent used for enhancing delivery of drug to tumor comprises imidazole compounds.
                                                                                                                                                                                                                                                                                                                                                                                                            Chen Z, Michaud SD, Wang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cadherin; cytostatic; gynecological; endometriosis; endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degeneration. The present sequence represents a cyclic pept classical cadherin cell adhesion recognition (CAR) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 34; DB 4; Length 5; 100.0%; Pred. No. 1.8e+06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclic peptide endothelial cell adhesion modulator #1.
                                                            'note= "N-terminal acetylation"
                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                            Gour BJ, Blaschuk OW, Ali A, Ni F,
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 146; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM47477 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                           (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                           24-JAN-2000; 2000US-00491078
                                                                                                                                                                                                                                                                24-JAN-2001; 2001WO-US002508
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es 5; Conserv
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                                                                                                                                                                WO200153331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5 AA;
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Modified-site
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                                                                                                                                                                                                             26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM47477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Ha Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes methods which have been developed for detecting and evaluating cancer that are based on the finding that OB-cadherin are expressed by metastatic carcinomae cells, but not by highly differentiated, poorly invasive carcinomae. A method for determining the presence or absence of a cancer in a patient comprises:

(1) conteacting a biological sample from the patient with a binding agent that specifically binds to OB- or N-cadherin OR with an oligonucleotide that specifically binds to OB- or N-cadherin or that hybridises to the binding agent of polymucleotide that binds to the binding agent of polymucleotide that binds to the binding agent of polymucleotide that things to the coligonucleotide, relative to a predetermined cut-off value, and off determining the present invention can be used to determine the methods from the present invention can be used to determine the metastatic potential of a cancer. The methods may be used to detect a metastatic potential of a cancer. The method sinclude leukemia, progression of a cancer, or to evaluate the metastatic potential of a cancer. Cancers which may be evaluated using the methods include leukemia, progression of a cancer, breast cancer and ovarian cancer. Affilial represent peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences used in the exemplification of the present invention. Specifically, AAY13503 to AAY13789 represent OB-cadherin cell adhesion recognition (CAR) peptides and AY373790 to AAY13808 represent N-cadherin CAR peptides. AAZ47906 to AAZ473190 to AAY13808 represent in examples
                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting expression of OB-cadherin or N-cadherin used for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h similarity 100.0%; Score 34; DB 3; Length 5; Similarity 100.0%; Pred. No. 1.8e+06; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclic peptide with classical cadherin CAR sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 21; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG65370 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                         (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                          Blaschuck OW, Gour BJ, Byers S;
                                                                                                                                                                                                                                         99US-00234395.
                                                                                                                                                                                         98US-00073040.
98US-00187859.
                                                                                                                                         99WO-CA000362
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evaluating cancer.
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Ното варіелв.
                                             WO9957565-A2
                                                                                                                                           05-MAY-1999;
                                                                                                                                                                                         05-MAY-1998;
06-NOV-1998;
                                                                                             11-NOV-1999.
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RESULT 8 AAG65370

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                                                                                                                                                                                                                                          The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
                                                                                                                                                                        Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metastasis, cancer; binding agent; cell adhesion recognition; CAR; OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;
        /note= "Linked to residue 1 to form a cyclic peptide, terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 5; Length 5; 100.0%; Pred. No. 1.8e+06; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-cadherin cell adhesion recognition sequence #1.
                                                                                                                                   Ali A;
                                                                                                                                    Farookhi R,
                                                                                                                                                                                                                        Claim 6; Page 64; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU60211 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00073040.
98US-00187859.
99US-00234395.
                                                                            09-APR-2001; 2001WO-US011669
                                                                                              07-APR-2000; 2000US-00544782
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                   Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
5, Conserv
                                                                                                                 (UYMC-) UNIV MCGILL
                                                                                                                                                       WPI; 2002-049129/06
                                                                                                                                                                                                                                                                                                                                           modulating peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS2002146687-A1.
                                      WO200177146-A2
                                                                                                                                                                                                                                                                                                                                                              Sequence 5 AA;
Modified-site
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06-NOV-1998;
20-JAN-1999;
                                                                                                                                    Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-2003
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                                                         18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU60211;
                                                                                                                                                                                                       sequence
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                                                                                                                                                                                                                                                                                                         Diagnosing or evaluating metastatic potential of cancer in patient by contacting biological sample obtained from patient with specified binding agent or oligonucleotide, and detecting polypeptide that binds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic; cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis; central nervous system; wound healing; vasopermeability; N-cadherin; demyelinating neurological disease; astrocyte; synaptic stability; ovary; neutgrowth; spinal cord injury; macular degeneration; bladder; melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia; immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -cadherin, respectively, CAR sequences
                                                                                                                                                                          Byers S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell adhesion recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 8; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO43539 standard; peptide; 5 AA.
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Query Match
Best Local Similarity 100.v.
Best Local Similarity
                                                                                                                                                                          Blaschuk OW, Symonds JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2003 (first entry)
   BLASCHUK O W.
                               SYMONDS J M.
BYERS S.
                                                                                                                                                                                                                                         WPI; 2003-255125/25
                                                                                                      (GOUR/) GOUR B J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002168761-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                binding agent
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(BLAS/)
(SYMO/)
(BYER/)
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Wang S;

Chen Z, Michaud SD,

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New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries.
                                                                                                                                                                                                                                                                                                                                 Claim 15; SEQ ID NO 10; 281pp; English.
                                                                                                                                                                                           Gour BJ, Blaschuk OW, Ali A, Ni F,
                                                                                                                                                               (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                       24-JAN-2000; 2000US-00491078.
24-JAN-2001; 2001US-00769145.
                                                                                            10-APR-2003; 2003US-00412701.
                                                                                                                                                                                                                                    WPI; 2004-268836/25.
                                        US2004058864-A1.
                                                                   25-MAR-2004
              Synthetic.
                                                                                                                                                                                                           Hu 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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ID AAG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        쉽
                                                                                                                                                                                                                                                                                     The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide ring. The agent that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadhesion in a mammal, for adhesion, for reducing unwanted cellular adhesion in a mammal, for caher, for inhibiting angiogenesis, for enhancing the delivery of a drug to a tumour, for inhibiting the cartral nervous system, for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for increasing wound healing, for enhancing migration of an N-cadherin expressing cell on astrocytes, facilitating migration of an N-cadherin expressing cell on astrocytes, for inhibiting spinal cord injuries and for treating mecular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agent is useful for treating skin disorders, acute B cell leukaemia. Excessive immune excessive immune excessive immune expensents a sadherin (CAD) cell adhesion recognition (CAR) sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer; angiogenesis; central nervous system; wound healing; foreign tissue adhesion; vasopermeability; demyelinating neurological disease; astrocyte; synaptic stability; neurite outgrowth; spinal cord injury; macular degeneration; metastasis; bladder; tumour; ovary; melanoma; carcinoma; leukaemia; multiple sclerosis; cytostatic; antiangiogenic; neuroprotective; ophthalmological; Cell adhesion-modulating peptidomimetic; cadherin cell adhesion recognition sequence; CAR; cyclic.
                                                                                                                                                                                                           intercellular adhesion, for enhancing wound healing, has threeddimensional structure of cyclic
                                                                                                                                                                                              Novel cell adhesion modulating agent for modulating cadherin-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                           Wang S;
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                                                                                                                           Michaud SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 7; I 100.0%; Pred. No. 1.8e+06;
                                                                                                                           Chen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                          Ali A, Ni F,
                                                                                                                                                                                                                                                                 Claim 15; Page 99; 309pp; English.
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                                                                                                                           Gour BJ, Blaschuk OW,
 GOUR B J.
BLASCHUK O W.
                                                                      ö
                                                                                                                                                                  WPI; 2003-521524/49.
                                                     CHEN Z.
MICHAUD S I
WANG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CHAVC 5
                            ALI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 AA;
                                                                                               HU Z.
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                                                                     (MICH/)
(WANG/)
(HUZZ/)
                            (ALIA/)
(NIFF/)
  (GOUR/)
                                                        (CHEN/)
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Matches
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The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, classical cadherin-mediated cell adhesion, modulating classical cadherin-mediated intercellular adhesion, reducing unwanted cellular adhesion in a mammal, enhancing the delivery of a drug to a tumour in a mammal, enhancing the delivery to the central nervous system of a mammal, enhancing drug delivery to the central nervous system of a mammal, enhancing drug delivery to the central nervous system of a mammal, enhancing drug delivery to the central nervous system of a mammal, increasing vound healing in a mammal, tenhancing adhesion of foreign tissue implanted within a mammal, candulating adhesion of foreign tissue implanted within a mammal, call mammal, increasing cell on astrocytes, inhibiting synaptic stability in a mammal, modulating meutite outgrowth, treating spinal cord injuries in a mammal, modulating macular candor in a mammal. The compounds are useful for inhibiting the development of cancer, e.g. treating corp preventing cancer and/or inhibiting anglogenesis, for enhancing the cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agents are also useful in inhibiting anglogenesis, for enhancing delivery of a drug to a tumour in a mammal, for enhancing delivery of a drug to a tumour in a mammal, for enhancing delivery of a drug to a tumour in a mammal, for enhancing wound healing a mammal, for modulating the immune system of a mammal, for modulating a mammal, for modulating and energenesis (such as multiple sclerosis) in a mammal, for modulating synaptic stability in a mammal, for modulating synaptic stability in a mammal, for contains and a mammal.

Contains and a mammal and a trug to a tumour in a mammal and a mammal and a mammal and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating macular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion-modulating peptidomimetic, comprising classical cadherin cell adhesion recognition (CAR) sequence.
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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Cyclic peptide with classical cadherin CAR sequence
                                                                                                                                                                                                                                                                                                                          24-JAN-2000; 2000US-00491078
                                                                                                                                                                                                                                                                                            24-JAN-2001; 2001WO-US002508
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                                                                                                                                                                                                                                                                                                                                                                                       Gour BJ, Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-549899/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHAVC 5
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                                                                                                                         Key
Modified-site
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                                                                                                                                                                                  Modified-site
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                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of vyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting angiogenesis, enhancing development of cancer, inhibiting angiogenesis, enhancing delivery to the CNS, enhancing wound healing, modulating the immune system, increasing vasopermeability, exating demyelinating disease, faciliteting migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating neurite outgrowth, and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with
                                                                                       Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell adhesion modulating agent used for enhancing delivery of drug to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michaud SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       classical cadherin cell adhesion recognition (CAR) sequence
                                                                                                                                                                                                                                                             /note= "putative C-terminal amide or ester"
                                                                                                                                                                                                                 /note= "putative N-terminal acetylation or alkoxybenzylation"
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                                                            Cyclic peptide with classical cadherin CAR sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor comprises imidazole compounds.
                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ali A,
                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2000; 2000US-00491078.
                                                                                                                                                                                                                                                                                                                                                        24-JAN-2001; 2001WO-US002508
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Best Local Similarity 100.v.
--an 5; Conservative
                              (first entry)
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                                                                                                                                                       Synthetic
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   AAG65445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu Z;
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ID AAG6
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AC AAG6
XX
DT 30-N
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The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidonimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing treating demyelinating the immune system, increasing vasopermeability, treating demyelinating disease, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating degeneration. The present sequence represents a cyclic peptide with classical cadherin cell adhesion recognition (CAR) sequence
Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion modulating agent used for enhancing delivery of drug to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "putative C-terminal amide or ester"
                                                                                                                                                                                                                                                                                                                                         'note= "putative N-terminal acetylation or
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100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   alkoxybenzylation"
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WPI; 2001-549899/61
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CHAVC
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6 AA;
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                                                                               26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG65450;
                                                                                                                                                               Gour BJ,
                                                                                                                                                                         Hu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
AAG65450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                        The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing claivery of a drug to a tumor, inhibiting development of cancer, inhibiting anglogenesis, enhancing drug delivery to the CMS, enhancing wound healing, modulating the immune system, increasing vasopermeability, treating demyelinating disease, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating energing cell and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell adhesion, imidazole, peptidomimetic, cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
                                                                                                                                                                                                                                                         Cell adhesion modulating agent used for enhancing delivery of drug to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                       Wang
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                                                                                                                                                                                                        Michaud SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 34; DB 4; Lengtn b; 100.0%; Pred. No. 1.8e+06; "....marches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclic peptide with classical cadherin CAR sequence.
                                                           'notes "N-terminal acetylation"
                                                                                                                                                                                                       Chen Z,
                                                                               /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                     tumor comprises imidazole compounds.
cerebroprotective; muscular; cyclic.
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                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                        Claim 15; Page 146; 436pp; English
                                                                                                                                                                                  (ADHE-) ADHEREX TECHNOLOGIES INC.
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                                                                                                                                                                                                       Ali A,
                                                                                                                                            24-JAN-2001; 2001WO-US002508.
                                                                                                                                                               24-JAN-2000; 2000US-00491078
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5, Conservative
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                                                                                                                                                                                                                                      WPI; 2001-549899/61.
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                                                                                                   WO200153331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6 AA;
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                                                                     Modified-site
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                    Synthetic
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Best Local S
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The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of eyello peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing treating demyelinating the immune system, increasing vasoperameability, treating demyelinating diesase, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating neurite cougrowth, and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with classical cadherin cell adhesion recognition (CAR) sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adhesion modulating agent used for enhancing delivery of drug to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang S;
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                                                                                                                /note= "putative C-terminal amide or ester"
/note= "putative N-terminal acetylation or alkoxybenzylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
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100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor comprises imidazole compounds.
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                                                                                                                                                                                                                                                                                                                         24-JAN-2001; 2001WO-US002508
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24-JAN-2001; 2001WO-US002508.
                                                                                    Gour BJ, Blaschuk OW,
Hu Z;
                                                                                                                     WPI; 2001-549899/61.
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                                                                                                                                                                                                                                                                                                                                                               Sequence 6 AA;
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Modified-site
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26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
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                                                                                                                                                                                                                                      The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing wound healing, modulating the immune system, increasing vasopermeability, treating demyelinating disease, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating meurite coutgrowth, and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with classical cadherin cell adhesion recognition (CAR) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
                                                                                                                                                                                    Cell adhesion modulating agent used for enhancing delivery of drug to tumor comprises imidazole compounds.
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                                                                                                                               Wang
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                                                                                                                               Chen Z, Michaud SD,
/note= "putative C-terminal amide or ester"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclic peptide with classical cadherin CAR sequence.
                                                                                                                               Ni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                    Example; Page 414; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG65448 standard; peptide; 6 AA.
                                                                                                           (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                               Ali A,
                                                               24-JAN-2001; 2001WO-US002508
                                                                                     24-JAN-2000; 2000US-00491078
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Best Local Similarity 100.00
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                               Gour BJ, Blaschuk OW,
                                                                                                                                                               WPI; 2001-549899/61
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                     WO200153331-A2
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Modified-site
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The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that compides a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting angiogenesis, enhancing delivery to the CMS, enhancing treating angiogenesis, enhancing delivery to the CMS, enhancing creating demyelihating disease, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating neurite outgrowth, and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with classical cadherin cell adhesion recognition (CAR) sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide. Linked to residue 1 to form cyclic peptide"
                                                                                                                                                                                                                                                                               Cell adhesion modulating agent used for enhancing delivery of drug to tumor comprises imidazole compounds.
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                                                                                                                         Wang
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                                                                                                                         Michaud SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                            Chen Z,
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                                                              (ADHE-) ADHEREX TECHNOLOGIES INC.
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                                                                                                                         Ali A,
24-JAN-2000; 2000US-00491078.
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The present invention relates to a method for modulating endothelial call adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogeneals, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting
                                                    Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Linked to residue 6 to form a cyclic peptide, terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Linked to residue 1 to form a cyclic peptide, terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cadherin; cytostatic; gynecological; endometriosis;
endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6;
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                                                                                                                                                        Claim 6; Page 64; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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                  WPI; 2002-049129/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      modulating peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6 AA;
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                                                                                                                                                                                                                                                                                           The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing tho development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence was used to illustrate the present invention
                                                                                                                                                          Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Linked to residue 1 to form a cyclic peptide, terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cadherin; cytostatic; gynecological; endometriosis; endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclic peptide endothelial cell adhesion modulator #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 34; DB 5; L 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blaschuk OW, Gour BJ, Farookhi R, Ali A;
                                                                               Ali A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                               Farookhi R,
                                                                                                                                                                                                                                                            Example 1; Page 49; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM47521 standard; peptide; 6 AA.
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  07-APR-2000; 2000US-00544782
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                                                                               Gour BJ
                                       (UYMC-) UNIV MCGILL.
                                                                                                                    WPI; 2002-049129/06.
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                           RESULT 23
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                                                 The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometricisis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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                                                                                                                                                                                                                      Gaps
cell with a cyclic peptide having cadherin cell adhesion recognition
                                                                                                                                                                                                                                                                                                                                                                                                  Cadherin; cytostatic; gynecological; endometriosis; endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
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                                                                                                                                                                                                 100.0%; Score 34; DB 5; Length 6; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Cyclic peptide endothelial cell adhesion modulator #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ali A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                               Disclosure; Page 5; 139pp; English
                                                                                                                                                                                                                                                                                                                  AAM47554 standard; peptide; 6 AA.
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                                                                                                                                                                                                                      5; Conservative
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                                                                                                                                                                                                             Local Similarity
                                                                                                                                                          modulating peptide
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The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells as a result of surgery, injury, chapter and inflammation. The present sequence is one such
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endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
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; Pred. No. 1.8e+06;
0; Mismatches 0;
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blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
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endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
cyclic.
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cadherin; cytostatic; gynecological; endometriosis; endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
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                                                                                                    Length 6;
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                                                                                                 100.0%; Score 34; DB 5; I 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0;
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                                                                           Query Match
Best Local Similarity 100.
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modulating peptide
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                                                       Sequence 6 AA;
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The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadherin-mediated intercellular adhesion, for reducing unwanted cellular adhesion in a mammal, for enhancing the delivery of a drug to a tumour, for inhibiting the central nervous system, for enhancing delivery to the central nervous system, for enhancing delivery to the central nervous system, for enhancing wound healing, for modulating the immune system of a mammal, for increasing the immune system of a mammal, for increasing assopermeability, for treating a demyelinating neurological disease, for facilitating migration of an N-cadherin expressing cell on astrocytes, continuiting synaptic stability, for modulating neurite outgrowth, for treating spinal cord injuries and for treating macular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or
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                                                                                                                                                                                                                                                                                             Cadherin, CAD; extracellular domain; cell adhesion; peptidomimetic; cander; angiogenesis; cander; angiogenesis; central nervous system; wound healing; vasopermeabiltty; N-cadherin; demyelinating neurological disease; astrocyte; synaptic stability; ovary; mentre outgrowth; spinal cord injury; macular degeneration; bladder; melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia; immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
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                 Gaps
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                                                                                                                                                                                                                                                                Classical cadherin CAR sequence cyclic peptide peptidomimetic #73
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               Indels
Pred. No. 1.8e+06; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                cell adhesion recognition sequence.
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                                                                                                                                                              ABO43613 standard; peptide; 6 AA.
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100.0%;
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Hu Z;
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BLASCHUK O W.
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MICHAUD S
WANG S.
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 Best Local
Matches
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(WANG/)
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                                                                                                                              RESULT 26
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leukaemia. The agent is useful for treating skin disorders, acute B cell leukaemia, excessive immune reactions involving the humoral immune system and generation of immunoglobulins and diseases associated with excessive generation of T cells. This sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
                                                                                                                                                                                                                                                                                                                                                                                                                      Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic; cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis; central nervous system; wound healing; wasopermeability, N-cadherin; demyelinating neurological disease; astrocyte; synaptic stability; ovary; neurite outgrowth; spinal cord injury; macular degeneration; bladder; immanogical; carcina; skin disorder; acute B cell leukaemia; immune reaction; immunoglobulin; T cell generation; CAR; cyclic; cell adhesion recognition sequence.
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                                                                                                                                                                   Gaps
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                                                                                                                                   100.0%; Score 34; DB 7; I 100.0%; Pred. No. 1.8e+06; iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                         ABO43610 standard; peptide; 6 AA.
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CHEN Z.
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Hu Z;
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cenhancing the delivery of a drug to a tumour, for inhibiting the development of cancer, for inhibiting angiogenesis, for enhancing drug development of cancer, for inhibiting angiogenesis, for enhancing drug calivery to the central nervous system. for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for woodulating the immune system of a mammal, for increasing enterological disease, for facilitating migration of an N-cabharin expressing cell on astrocytes, for inhibiting synaptic stability, for modulating neurite outgrowth, for treating spinal cord injuries and for treating macular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agent is useful for treating skin disorders, acute B cell leukaemia, excessive immune reactions involving the humoral immune system and generation of immunoglobulins and diseases associated with excessive generation of Immunoglobulins and diseases associated with excessive dehesion recognition (CAR) sequence represents a cadherin (CAD) cell
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Best Local Similarity 100..
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BLASCHUK O W.
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MICHAUD S D.
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The invention relates to a cell adhesion modulating agent which is a comprises the sequence HAV within a cyclic peptide ring. The agent that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadhesion in a mammal, for adhesion, for reducing unwanted cellular adhesion in a mammal, for adhesion, for reducing unwanted cellular adhesion in a mammal, for cahencing the delivery of a drug to a tumour, for inhibiting the central nervous system, for analysems of cancer, for inhibiting analysement of cancer, for inhibiting analysement of cancer, for inhibiting analysement of cancer in a mammal, for modulating the adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for increasing cell on astrocytes, cancer is a bladder tumour, overlan tumour, advanced regeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or cancer is a mammal diseases associated with excessive and generation of rells. This sequence represents a cadherin (CAD) cell cancer or adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
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dimensional structure similar to three-dimensional structure of cyclic
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                                                        Disclosure; Page 7; 309pp; English.
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BLASCHUK O W.
ALI A.
NI F.
CHEN Z.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6 AA;
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(CHEN/)
(MICH/)
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(ALIA/)
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(GOUR/)
                                                                           ALIA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a cell adhesion modulating agent which is a peptidominetic having a three-dimensional structure of a cyclic peptide that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadherin-mediated intercellular adhesion, for reducing unwanted cellular adhesion in a mammal, for enhancing the delivery of a drug to a tumour. for inhibiting the development of cancer, for inhibiting angiogenesis, for enhancing delivery to the central nervous system, for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for increasing vasopermeability, for treating a demyelinating neurological disease, for facilitating migration of an N-cadherin expressing cell on astrocycles, for inhibiting synaptic stability, for modulating meular degeneration. The cancer is a bladder tumour, ovarian tumour, malanoma, carcinoma or leukaemia, accessive immune reactions involving the humoral immune system cand generation of Immunoglobulins and diseases associated with excessive generation recognition (CAR) sequence represents a cadherin (CAD) cell
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                                                                                                 Novel cell adhesion modulating agent for modulating cadherin-mediated intercellular adhesion, for enhancing wound healing, has threedimensional structure similar to three-dimensional structure of cyclic
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                                      Chen Z, Michaud SD,
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                                      Ali A, Ni F,
                                                                                                                                                                 Disclosure; Page 7; 309pp; English
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Best Local Similarity 100...
5; Conservative
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                                      Gour BJ, Blaschuk OW,
                                                                           WPI; 2003-521524/49.
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 WANG S.
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             HU Z.
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(WANG/)
             (HUZZ/)
                                                                                                                                          peptide
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The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide that comprises the sequence HAV within a cyclic peptide ring. The agent that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadherin-mediated intercellular adhesion, for reducing unwanted cellular adhesion in a mammal, for enhancing the delivery of a farug to a tumour. for inhibiting the delivery of a inhibiting angiogenesis, for enhancing drug development of cancer, inhibiting angiogenesis, for enhancing drug cellivery to the central nervous system, for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the adhesion of foreign tissue implanted within a mammal, for containing the immune system of a mammal, for increasing vasopermeability, for treating a demyelinating neurological disease, for for inhibiting synaptic stability, for modulating neurite outgrowth, for treating spinal cord injuries and for treating macular degeneration. The cancer is a bladder tumour, newar, melanoma, carcinoma or leukaemia, excessive immune reactions involving the humoral immune system and generation of T cells. This sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel cell adhesion modulating agent for modulating cadherin-mediated intercellular adhesion, for enhancing wound healing, has threedimensional structure similar to three-dimensional structure of cyclic
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24-JAN-2001; 2001US-00769145.
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BLASCHUK O
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MICHAUD
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(CHEN/)
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The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide ring:

that comprises the sequence HAV within a cyclic peptide ring:

that comprises the sequence HAV within a cyclic peptide ring:

adhesion, for reducing unwanted cellular adhesion in a mammal, for adhesion, for reducing unwanted cellular adhesion in a mammal, for cancer, for inhibiting the adhesion of cancer, for inhibiting wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for increasing

callivery to the central nervous system, for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for cancer in a mammal ord injuries a demyelinating neurological disease, for facilitating migration of an N-cadharin expressing cell on astrocytes, for inhibiting spinal cord injuries and for treating mcurite outgrowth, for treating spinal cord injuries and for treating mcular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia, excessive immune reactions involving the humoral immune system and generation of immunoglobulins and diseases associated with excessive and generation of calls. This sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence ceptesents a cadherin (CAD) cell
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melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia; immune reaction; immunoglobulin; T cell generation; CAR; cyclic; cell adhesion recognition sequence.
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Hu Z;
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BLASCHUK O W.
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CHEN Z.
MICHAUD S D.
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                                                                               Synthetic.
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Length 6;
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100.0%; Score 34; DB 7; I
100.0%; Pred. No. 1.8e+06;
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Sequence 6 AA

ADK13619 standard; peptide; 6 AA.

RESULT 32 ADK13619 ID ADK1 XX ADK1

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ADK13619

Local Similarity 100. nes 5; Conservative

Matches

Query Match

CHAVC 5

The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, identifying a compound that modulates classical cadherin-mediated cell adhesion, modulating classical cadherin-mediated intercellular adhesion, cadhesion a tumour in a mammal, enhancing the delivery of a drug to a tumour in a mammal, enhancing the delivery concert in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery to the central nervous system of a mammal, enhancing drug delivery to the central nervous system of a mammal, enhancing delivery concert in a mammal enhancing wound healing in a mammal, enhancing adenyelinating neurological disease in a mammal, cadolating an activation of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability in a mammal, modulating neurite outgrowth, treating spinal cord injuries in a mammal, modulating neurite outgrowth, treating spinal cord injuries in a mammal, modulating neurite outgrowth, treating spinal cord injuries in a mammal, modulating neurite outgrowth, configuration cancer and/or inhibiting metateasis. The cancer, e.g. treating agents are useful for inhibiting angiogenesis, for enhancing the drug to a tumour in a mammal, for enhancing delivery contral nervous system of a mammal, for enhancing adhesion of foreign tissue implanted within a configuration neural nervous system of a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for modulating phenetic guestility in a mammal, for modulating or treating spinal cord inhibiting synaptic stability in a mammal, for modulating synaptic stability in a mammal, for modulating spinal cord inhibiting synaptic stability in a mammal, for modulating spinal cord inhibiting synaptic stability in a mammal secondarial secondarial secondarial secondarial secondar demyelinating neurological disease, astrocyte, synaptic stability; neurite outgrowth, spinal cord injury; macular degeneration; metastasis; bladder; tumour; ovary; melanoma; carcinoma; leuksemia; multiple sclerosis; cytostatic; antiangiogenic; neuroprotective; ophthalmological; Cell adhesion-modulating peptidomimetic; cadherin cell adhesion recognition sequence; CAR; cyclic. New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastagis, inhibiting anglogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries. Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer; anglogenesis; central nervous system; wound healing; foreign tissue adhesion; vasopermeability; treating macular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion-modulating peptidomimetic, comprising classical cadherin cell adhesion recognition (CAR) sequence. Wang S; Cadherin-mediated cell adhesion-modulating peptidomimetic #78. Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Disclosure; SEQ ID NO 85; 281pp; English. (ADHE-) ADHEREX TECHNOLOGIES INC. 10-APR-2003; 2003US-00412701. 24-JAN-2000; 2000US-00491078. 24-JAN-2001; 2001US-00769145. (first entry) WPI; 2004-268836/25. US2004058864-A1. 17-JUN-2004 25-MAR-2004 Synthetic. Hu Z; 

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The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, identifying a compound that modulates classical cadherin-mediated cell adhesion, modulating classical cadherin-mediated intercellular adhesion, adhesion, modulating classical cadherin-mediated intercellular adhesion, reducing unwanted cellular adhesion in a mammal, enhancing the delivery of a drug to a tumour in a mammal, inhibiting the development of a cancer in a mammal, inhibiting adhesion of a mammal, enhancing drug delivery control never the central nervous system of a mammal, increasing vesopermeability in a mammal, treating the immune system of a mammal, increasing vesopermeability in a mammal, treating a demyelinating neurological disease in a mammal, and mammal, treating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability in a mammal and treating macular treating macular cadherin-mediated cell adhesion. The coll adhesion modulating or enhancing cadherin-mediated cell adhesion. The cell adhesion modulating agents are useful for inhibiting the development of cancer, e.g. treating
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                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis; central nervous system; wound healing; foreign tissue adhesion; vasopermeability; demyelinating neurological disease; astrocyte; synaptic stability; neurite outgrowth; spinal cord injury; macular degeneration; metastasis; bladder; tumour; ovary; melanoma; carcinoma; leukaemia; multiple sclerosis; cycotatic; antianglogenic; neuroprotective; ophthalmological; Cell adhesion-modulating peptidomimetic; cadherin cell adhesion recognition sequence; CAR; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries.
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                    100.0%; Score 34; DB 8; Length 6; 100.0%; Pred. No. 1.8e+06;
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Hu Z;
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or preventing cancer and/or inhibiting metastasis. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agents are also useful in inhibiting angiogenesis, for enhancing the delivery of a drug to a tumour in a mammal, for enhancing drug delivery to the central nervous system of a mammal, for enhancing wound healing in a mammal, for modulating the immune system of a mammal, for treating a dhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for treating a demyelinating neurological disease (such as multiple sclerosis) in a mammal, for inhibiting synaptic stability in a mammal, for modulating neurological disease (such as multiple sclerosis) in a remain eutgrowth, for treating spinal cord injuries in a mammal and for treating macular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion recognition (CAR) sequence.
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer; angiogenesis; central nervous system; wound healing; foreign tissue adhesion; vasopermeability; demyclinating neurological disease; astrocyte; synaptic stability; neurite outgrowth; spinal cord injury; macular degeneration; metastasis; bladder; tumour; ovary; melanoma; carcinoma; leuksemia; multiple sclerosis; cytostatic; antianglogenic; neuroprotective; ophthalmological; cell adhesion-modulating peptidomimetic; cadherin cell adhesion recognition sequence; CAR; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion,
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cadherin-mediated cell adhesion-modulating peptidomimetic #82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD,
                                                                                                                                                                                                                                                                                                                      100.0%; Score 34; DB 8; Length 6; 100.0%; Pred. No. 1.88+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK13623 standard; peptide; 6 AA.
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24-JAN-2001; 2001US-00769145.
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                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CHAVC 5
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                                                                                                                                                                                                                                                                                              Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                       Query Match
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ADK13623
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                                                                                                                                                                                                                                                      treating macular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a classical cadherin cell adhesion recognition (CAR) sequence.
compound that modulates classical cadherin-mediated cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cadherin-mediated cell adhesion-modulating peptidomimetic #74.
                                                                                                                                                                                                                                                                                                                   100.0%; Score 34; DB 8; Length 6; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK13615 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2000; 2000US-00491078.
24-JAN-2001; 2001US-00769145.
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                             1 CHAVC 5
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                                                                                                                                                                                                                                                                                                  Sequence 6 AA;
 identifying a
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The invention relates to a ceri adnession-modutating agent. The invention cases to a cere and a candidated compound for the ability to modulate classical cadherin-mediated cell adhesion, identifying a compound that modulates classical cadherin-mediated cell adhesion, adhesion, modulating classical cadherin-mediated intercellular adhesion, reducing unwanted cellular adhesion in a mammal, enhancing the delivery of a drug to a tumour in a mammal, enhancing the delivery concerns and adhesion of foreign tissue implanted within a mammal, enhancing drug delivery concerns in entraing adhesion of foreign tissue implanted within a mammal, enhancing adhesion of foreign tissue implanted within a mammal, contains a demyelinating neurological disease in a mammal, concerns a mammal, treating a demyelinating neurological disease in a mammal, concernsability in a mammal, modulating vasopernseability in a mammal, modulating or inhibiting synaptic stability in a mammal, modulating or chancing cadherin-mediated cell adhesion. The cell adhesion modulating or enhancing cadherin-mediated cell adhesion. The cell adhesion modulating or concerns are also useful in inhibiting angiogenesis, for enhancing the development of cancer, is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agents are alseful in inhibiting angiogenesis, for enhancing delivery of a tumour in a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for endulating the immune system of a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for modulating panestic stability in a mammal, for modulating energy in a mammal, for modulating synaptic stability in a mammal, for modulating synaptic in a mammal in a mamma
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                                                                                                                       New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries.
                                                                                                                                                                                                                                                                                                                    invention relates to a cell adhesion-modulating agent. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating macular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a classical cadherin cell adhesion recognition (CAR) sequence.
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     Wang S;
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     Chen Z, Michaud SD,
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100.0%; Pred. No. 1.8e+06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                   Claim 15; SEQ ID NO 81; 281pp; English.
        Ni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK13624 standard, peptide; 6 AA.
Gour BJ, Blaschuk OW, Ali A,
Hu Z;
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Matches 5; Conservative
                                                                                   WPI; 2004-268836/25.
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The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, idinity to modulate classical cadherin-mediated cell adhesion, dentifying a compound that an dential, enhancing the devicery of adhesion, modulating classical cadherin-mediated cell adhesion, modulating classical cadherin-mediated intercellular adhesion, creduting unwanted cellular adhesion, in a mammal, enhancing the devicery of a drug to a tumour in a mammal, inhibiting the development of a cancer in a mammal inhibiting adhesion of foreign tissue implanted within a mammal, contained adhesion of foreign tissue implanted within a mammal, contained and camperation of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability in a mammal and treating metrocytes, contained and central metrocytes in a mammal. The compounds are useful for inhibiting or cenhancing cadherin-mediated cell adhesion. The cell adhesion modulating the cancer, e.g. treating agents are useful for inhibiting metastasis. The cancer is a comman, for enhancing adherin-mediated cell adhesion in a mammal, for enhancing delivery of a drug to a tumour, melanoma, carcinoma or leukaemia. The agents are also useful in inhibiting angiogenesis, for enhancing delivery of a drug to a tumour in a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for enhancing adhesion of foreign tissue implanting a commission in a mammal, for modulating spinal cod injuries in a mammal, for modulating spinal cod injuries in a mammal, for modulating spinal cod injuries in a mammal, for companies and for a capilla adhesion in a mammal, for modulating spinal cod injuries in a mammal, for companies and codenies are also useful in a mammal or a mammal, for modulating spinal cod injuries in a mammal, for modulating spinal codenies are also useful adhesion and mammal and for
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                                                                                                                                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                   Chen Z, Michaud SD,
cadherin cell adhesion recognition sequence; CAR; cyclic.
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                                                                                                                                                                                                                                                                                                                                                   Ni F,
                                                                                                                                                                                                                                                                                                        (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                   Ali A,
                                                                                                                                                                                                                                 24-JAN-2000; 2000US-00491078.
24-JAN-2001; 2001US-00769145.
                                                                                                                                                                                      10-APR-2003; 2003US-00412701
                                                                                                                                                                                                                                                                                                                                       Gour BJ, Blaschuk OW,
Hu Z;
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                                                                                            US2004058864-A1.
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                                              Synthetic
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Gaps
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           Length 6;
                                  0; Indels
         100.0%; Score 34; DB 8; I 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
5; Conservative
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ADK13618 ID ADKI

ADK13618 standard; peptide; 6 AA.

CHAVC 5 CHAVC 5 RESULT 37 8 셤

ADK13618;

(first entry) 17-JUN-2004 Cadherin-mediated cell adhesion-modulating peptidomimetic #77.

Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer; angiogenesis; central nervous system; wound healing; foreign tissue adhesion; vasopermeability; demyelinating neurological disease; astrocyte; synaptic stability; neurite outgrowth; spinal cord injury; macular degeneration; metastasis; baldder; tumour; ovary; melanoma; carcinoma; leuksemia; multiple sclerosis; cytostatic; antiangiogenic; neuroprotective; ophthalmological; Cell adhesion-modulating peptidomimetic; cadherin cell adhesion recognition sequence; CAR; cyclic.

Synthetic.

US2004058864-A1.

25-MAR-2004.

10-APR-2003; 2003US-00412701.

24-JAN-2000; 2000US-00491078. 24-JAN-2001; 2001US-00769145.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Wang S; Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Hu 2;

WPI; 2004-268836/25.

New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries.

Disclosure; SEQ ID NO 84; 281pp; English.

The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, identifying a compound that modulates classical cadherin-mediated cell adhesion, adhesion, modulating classical cadherin-mediated intercellular adhesion, catherin in a mammal, enhancing the delivery of a drug to a tumour in a mammal, inhibiting angiogenesis in a mammal, enhancing delivery of a drug to a tumour in a mammal, enhancing delivery of to the central nervous system of a mammal, enhancing delivery of to the central nervous system of a mammal, increasing vasopermeability in a mammal, treating a demyelinating neurological disease in a mammal, modulating the immune system of a mammal, increasing vasopermeability in a mammal, treating admiration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability in a mammal and treating meuric outgrowth, treating spinal cord injuries in a mammal and treating meuric outgrowth, treating spinal cord injuries in a mammal and treating meuric outgrowth, treating spinal cord injuries in a mammal and treating meuric outgrowth, creating cadherin-mediated cell adhesion. The cell adhesion modulating agents are useful for inhibiting metastasis. The cancer, e.g. treating agents are useful for inhibiting metastasis. The cancer is a contex are also useful in inhibiting angiogenesis, for enhancing the delivery of a drug to a tumour in a mammal, for enhancing within a mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for enhancing a mammal, for modulating the immune system of a mammal, for madulating the immune system of a mammal, for modulating the immune system of a demyelinating neurological disease (such as multiple sclerosis) in a mammal, for inhibiting synaptic stability in a mammal, for modulating neurite outgrowth, for treating spinal cord injuries in a mammal and for treating macular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a classical cadherin cell adhesion recognition (CAR) sequence.

Indela

Pred. No. 1.8e+06; Mismatches 0;

100.04;

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Best Local Similarity
         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV.

The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting angiogenesis, enhancing development of cancer, inhibiting angiogenesis, enhancing development of cancer, inhibiting angiogenesis, enhancing development of cancer, creating demyelinating disease, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating neurite outgrowth, and treating spinal cord injuries and macular neurite coargrowth. The present sequence represents a cyclic peptide with classical cadherin cell adhesion recognition (CAR) sequence
                                                       ö
                                                                                                                                                                                                                                                Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell adhesion modulating agent used for enhancing delivery of drug to tumor comprises imidazole compounds.
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                            /note= "putative C-terminal amide or ester"
                                                                                                                                                                                                                                                                                                                                        /note= "putative N-terminal acetylation or alkoxybenzylation"
                                 Length 6;
                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michaud
                                                                                                                                                                                                                           Cyclic peptide with classical cadherin CAR sequence
                               100.0%; Score 34; DB 8; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ni F,
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 413; 436pp; English.
                                                                                                                                                          AAG65447 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gour BJ, Blaschuk OW, Ali A,
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                                                                                                                                                                                                      (first entry)
                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-549899/61.
                              Query Match
Best Local Similarity
                                                                            1 CHAVC 5
                                                                                                  1 CHAVC 5
           Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                 AAG65447;
                                                       Matches
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100.0%; Score 34; DB 4; Length 7;

Query Match

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The invention relates to cell adhesion modulating agents that comprise imidazole compounds of specified formulae that are peptidomimetics of cyclic peptides. The peptidomimetics have a structure similar to that of a cyclic peptide that comprises a cadherin cell recognition sequence HAV. The agents are used for modulating classical cadherin mediated intercellular adhesion, reducing unwanted cellular adhesion, enhancing delivery of a drug to a tumor, inhibiting development of cancer, inhibiting anglogenesis, enhancing drug delivery to the CMS, enhancing wound healing, modulating the immune system, increasing vasopermeability, treating demyelinating disease, facilitating migration of an N-cadherin expressing cell on astrocytes, inhibiting synaptic stability, modulating energite outgrowth, and treating spinal cord injuries and macular degeneration. The present sequence represents a cyclic peptide with classical cadherin cell adhesion recognition (CAR) sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR; cytostatic; vulnerary; immunomodulator; vasotropic; neuroprotective; cerebroprotective; muscular; cyclic.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclic peptide with classical cadherin CAR sequence.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                  AAG65446 standard, peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2001; 2001WO-US002508
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Best Local Similarity 100.
Matches 5; Conservative
5; Conservative
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                                                         1 CHAVC 5
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                                                                                                                                                                                                                                                                                                                            AAG65446;
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                                                                                                                                                                                                        RESULT 39
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/note= "Linked to residue 7 to form a cyclic peptide,

terminal CH3-SO2 group'

Location/Qualifiers

(first entry)

/note= "Linked to residue 1 to form a cyclic peptide, C-terminal amide"

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Cadherin; cytostatic; gynecological; endometriosis; endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
                                                                                Cyclic peptide endothelial cell adhesion modulator #39
           AAM47563 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                  07-APR-2000; 2000US-00544782
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                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                             Modified-site
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                                                         12-FEB-2002
                                                                                                                                                                                                                                                                                                      18-OCT-2001
                                                                                                                                                        Synthetic.
                                   AAM47563;
                                                                                                                                 cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometrisosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, modulating perideses and inflammation. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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                                                                                                                                                                                                                                                                                                      /note= "Linked to residue 1 to form a cyclic peptide,
                                                                                                                                                                                                                                                                  /note= "Linked to residue 7 to form a cyclic peptide, terminal acetyl or N-terminal CH3-SO2 group"
                                                                                                                                                                      Cadherin; cytostatic; gynecological; endometriosis;
endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 34; DB 5; Length 7; Local Similarity 100.0%; Pred. No. 1.8e+06; es 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                              Cyclic peptide endothelial cell adhesion modulator #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ali A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farookhi R,
                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                       AAM47556 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                   terminal amide
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                                                                                                                      12-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYMC-) UNIV MCGILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulating peptide
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CHAVC
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                                                                                                                                                                                                                    Synthetic
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Best Local S:
Matches 5;
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                                                                                               AAM47556;
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Ali A;

Farookhi R,

Gour BJ,

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                                                                                                                                                                                                              The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprises contacting an endothelial cell with a modulating peptide comprises.

The method is adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                          Disclosure; Page 5; 139pp; English.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulating peptide
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AAM47557
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AC AAM
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Gaps

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CHAVC 5

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CHAVC

RESULT 41

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US2002168761-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
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                                                                                                                   14-NOV-2002
                                                                             Synthetic.
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                                                                                                                                                                                                                                                                     Gour BJ,
                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                             (MICH/)
                                                                                                                                                                            (GOUR/)
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                                                                                                                                                                                                                                                  (HUZZ/)
                                                                                                                                                                                       (BLAS/
                                                                                                                                                                                                                                                                              Hu Z;
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8:
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                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
                                                                                                                                                                                                                                                                                                                      Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
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                                                                                                                   /note= "Linked to residue 7 to form a cyclic peptide, terminal acetyl or N-terminal CH3-SO2 group"
                                                                                                                                              /note= "Linked to regidue 1 to form a cyclic peptide, terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Classical cadherin CAR sequence cyclic peptide peptidomimetic #76.
                                      Cadherin; cytostatic; gynecological; endometriosis;
endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                  Cyclic peptide endothelial cell adhesion modulator #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 34; DB 5; L
100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                               Ali A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                Farookhi R,
                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO43616 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 64; 139pp; English.
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                                                                                                                                                                                                                      09-APR-2001; 2001WO-US011669.
                                                                                                                                                                                                                                          07-APR-2000; 2000US-00544782.
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 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                 Gour BJ,
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                                                                                                                                                                                                                                                              (UYMC-) UNIV MCGILL.
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                                                                                                                                                                                WO200177146-A2
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                                                                                                 Key
Modified-site
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                                                                                                                                                                                                                                                                                Blaschuk OW,
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 12-FEB-2002
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                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                     sequence.
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Best Local
                                                            cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO43616
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The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadherin-mediated intercellular adhesion, for reducing unwanted cellular adhesion in a mammal, for adhesion, for cancer, for inhibiting angiogenets of cancer, for inhibiting angiogenets of cancer, for inhibiting wound healing, for chancing the adhesion of foreign tissue implanted within a mammal, for cancer in the immune system of a mammal, for increasing wound healing, for condulating the immune system of a mammal, for increasing cancer is a not cancer, for inhibiting synaptic stability, for modulating neurological disease, for for inhibiting synaptic stability, for modulating mecular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia, excessive immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                 ovary;
cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis; central nervous systems; wound healing; vasopermeability; N-cadherin; demyelinating neurological disease; astrocyte; synaptic stability; ovarneurite outgrowth; spinal cord injury; macular degeneration; bladder; melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia; immunoglobulin; T cell generation; CAR; cyclic; ell adhesion recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel cell adhesion modulating agent for modulating cadherin-mediated intercellular adhesion, for enhancing wound healing, has three-dimensional structure similar to three-dimensional structure of cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Similarity 100.0%; Score 34; DB 7; L
Similarity 100.0%; Pred. No. 1.8e+06;
5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 309pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2001; 2001US-00769145.
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BLASCHUK (
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MICHAUD S
WANG S.
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Length 7;

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cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis; central nervous system, wound healing; vasopermeability; N-cadherin; demyelinating neurological disease; astrocyte; synaptic stability; ovary; neurite outgrowth; spinal cord injury; macular degeneration; bladder; melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia; immune reaction; immunoglobulin; T cell generation; CAR; cyclic; cell adhesion recognition sequence.
                                                                           Cadherin, CAD; extracellular domain; cell adhesion; peptidomimetic;
                                                           Classical cadherin CAR sequence cyclic peptide peptidomimetic #75.
                                                                                                                                                                                                                                                                                                                     Chen Z, Michaud SD,
                                                                                                                                                                                                                                                                                                                    Ni F,
        ABO43615 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                      Ali A,
                                                                                                                                                                                                        24-JAN-2001; 2001US-00769145.
                                                                                                                                                                                                                         24-JAN-2000; 2000US-00491078.
                                          (first entry)
                                                                                                                                                                                                                                                                                                                      Blaschuk OW,
                                                                                                                                                                                                                                          GOUR B J.
BLASCHUK O W.
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                                                                                                                                                                                                                                                                                                                                             WPI; 2003-521524/49.
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                                                                                                                                                                                                                                                                   NI F.
CHEN Z.
MICHAUD S
WANG S.
                                                                                                                                                                       JS2002168761-A1.
                                        25-SEP-2003
                                                                                                                                                                                        14-NOV-2002
                                                                                                                                                      Synthetic.
                         ABO43615;
                                                                                                                                                                                                                                                                                                                      Gour BJ,
                                                                                                                                                                                                                                                                                    (MICH/)
                                                                                                                                                                                                                                          GOUR/)
                                                                                                                                                                                                                                                                                                     (HUZZ/)
                                                                                                                                                                                                                                                   BLAS/
                                                                                                                                                                                                                                                           ALIA/
                                                                                                                                                                                                                                                                             CHEN/
                                                                                                                                                                                                                                                                                                                              Hu Z;
ABO43615
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The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide that that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadherin-mediated intercellular adhesion, for reducing unwanted cellular adhesion in a mammal, for enhancing the delivery of a drug to a tumour, for inhibiting the centeral nervous system, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the adhesion of foreign tissue implanted within a mammal, for modulating the adhesion of foreign tissue implanted within a mammal, for containing the immune system of a mammal, for increasing wasopermeability, for treating a demyelinating neurological disease, for facilitating migration of an N-cadherin expressing cell on astrocytes, for inhibiting synaptic stability, for modulating neurite outgrowth, for treating spinal cord injuries and for treating macular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or cancer is a bladder tumour ovarian tumour, melanoma, carcinoma or leukaemia, excessive immunoglobuling and diseases associated with excessive melanoma or and generation of immunoglobuling and diseases associated with excessive generation of T cells. This sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the Novel cell adhesion modulating agent for modulating cadherin-mediated intercellular adhesion, for enhancing wound healing, has threedimensional structure similar to three-dimensional structure of cyclic Disclosure; Page 7; 309pp; English. peptide.

Sequence 7 AA;

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The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, identifying a compound that modulates classical cadherin-mediated cell adhesion, modulating classical cadherin-mediated intercellular adhesion, adhesion, modulating classical cadherin-mediated intercellular adhesion, cadhesion, modulating classical cadherin-mediated cell cadherin-mediated cell cadherin-mediated intercellular adhesion, correcting unwanted cellular adhesion in a mammal, enhancing adhesion of a mammal, enhancing adhesion of foreign tissue implanted within a mammal, cort cort cortical cadhering admension of a mammal, increasing vasopermeability in a mammal, treating a demyelinating neurological disease in a mammal, contintitity in a mammal, modulating synaptic stability in a mammal, modulating meurite outgrowth, creating spinal cord injuries in a mammal and treating macular contintities in a mammal and treating macular cenhancing cadherin-mediated cell adhesion. The call adhesion modulating agents are useful for inhibiting the development of cancer, e.g. treating agents are useful for inhibiting the development of cancer, e.g. treating cort preventing cancer and/or inhibiting metastasis. The cancer is a
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; central nervous system; wound healing; foreign tissue adhesion; vasopermeability; demyelnating neurological disease; astrocyte; synaptic stability; neurite outgrowth; spinal cord injury; macular degeneration; metastasis; bladder; tumour; ovary; melanoma; carcinoma; leukaemia; ophthalmological; cyrostatic; antiangiogenic; neuroprotective; ophthalmological; cell adhesion-modulating peptidomimetic; cadhesion recognition sequence; CAR; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastais, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injutes.
                                                                                                                                                                                                                                                                                                                                                                                    adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
                                         Gaps
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                                                                                                                                                                                                                                                                                                                                               Cadherin-mediated cell adhesion-modulating peptidomimetic #79.
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                                         Indels
                                         ..
, DB 7; L
    Score 34; DB pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gour BJ, Blaschuk OW, Ali A, Ni F,
                                                                                                                                                                                                                          ADK13620 standard; peptide; 7 AA.
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    100.0%;
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24-JAN-2001; 2001US-00769145.
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                                                                                                                                                                                                                                                                                                       (first entry)
                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-268836/25.
  Query Match
Best Local Similarity
Matches 5, Conserv
                                                                                                                    CHAVC 5
                                                                                   1 CHAVC 5
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Wang

us-10-632-678-10.rag

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bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agents are also useful in inhibiting anglogenesis, for enhancing the delivery of a drug to a tumour in a mammal, for enhancing drug delivery to the central nervous system of a mammal, for enhancing wound healing in a mammal, for modulating the immune system of a mammal, for treating a demyelinating neurological disease (such as multiple solerosis) in a mammal, for inhibiting synaptic stability in a mammal, for modulating neurological disease (such as multiple solerosis) in a neurite outgrowth, for treating spinal cord injuries in a mammal and for treating amoular degeneration in a mammal. This sequence represents a cadherin-mediated cell adhesion-modulating peptidonimetic, comprising a classical cadherin cell adhesion recognition (CAR) sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer; angiogenesis; central nervous system; wound healing; foreign tissue adhesion; vacopermeability; demyelinating neurological disease; astrocyte; synaptic stability; neurite outgrowth; spinal cord injury; macular degeneration; metastasis; bladder; tumour; ovary; melanoma; carcinoma; leukaemia; multiple sclerosis; cytostatic; antiangiogenic; neuroprotective; ophthalmological; Cell adhesion-modulating peptidomimetic; cadherin cell adhesion recognition sequence; CAR; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cell adhesion modulating agent, useful for treating or preventing cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing wound healing, treating a demyelinating neurological disease or treating spinal cord injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a cell adhesion-modulating agent. The invention also relates to methods for screening a candidate compound for the ability to modulate classical cadherin-mediated cell adhesion, identifying a compound that modulates classical cadherin-mediated cell
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cadherin-mediated cell adhesion-modulating peptidomimetic #80.
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                                                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 8; L 100.0%; Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ali A, Ni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK13621 standard; peptide; 7 AA.
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24-JAN-2001; 2001US-00769145.
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                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                         Sequence 7 AA;
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to the central nervous system of a mammal, enhancing who welver the central nervous system of a mammal, enhancing adhesion of foreign tissue implanted within a mammal, enhancing adhesion of foreign tissue implanted within a mammal, amodulating the immune system of a mammal, increasing vasopermeability in a mammal, increasing vasopermeability in a mammal, increasing vasopermeability in a mammal, modulating enlar of activities in a mammal, modulating macular creating spinal cord injuries in a mammal and treating macular creating spinal cord injuries in a mammal and treating macular creating spinal cord injuries in a mammal and treating macular creating selected for inhibiting the development of cancer, e.g. treating or enhancing cancer and/or inhibiting metastasis. The cancer is a correst cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agents are also useful in inhibiting anglogenesis, for enhancing delivery cto the central nervous system of a mammal, for enhancing daily and mammal, for enhancing adhesion of foreign tissue implanted within a mammal, for enhancing adhesion of foreign tissue implanted within a cammmal, for inhibiting synaptic stability in a mammal, for modulating or treating macular degenerating spinal cord injuries in a mammal or treating macular degeneration in a mammal. This sequence represents a cacherin-mediated cell adhesion-modulating peptidomimetic, comprising a cacherin-mediated cell adhesion recognition (CAR) sequence.
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                    reducing unwanted cellular adhesion in a mammal, enhancing the delivery of a drug to a tumour in a mammal, inhibiting the development of a cancer in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
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adhesion, modulating classical cadherin-mediated intercellular adhesion,
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terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 8; Length 7; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclic peptide endothelial cell adhesion modulator #22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM47562 standard; peptide; 8 AA.
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Best Local Similarity
5; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
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Modified-site
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the Kunitz protease inhibitors (RPI) domain of the amyloid precursor the Kunitz protease inhibitors can be used used to treat or prevent corporters associated with increased activity of serine proteases inhibitors can be used used to treat or prevent disorders associated with increased activity of serine proteases.

Co bypass surgery where plasma proteases are activated by contact with surfaces in the heart-lung machine), but also other conditions such as pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis; myocardial infarction; and transplant rejection. They are also for organ preservation and to promote wound healing. In vitro the protease cinhibitors may be used to inhibit serine proteases during preparation of cell extracts. The protease inhibitors are based on a human peptide sequence so are unlikely to be immunogenic, can be produced at high levels in recombinant expression systems, and can inhibit a wide range of serine proteases. They are more potent or specific than known inhibitors. The present sequence represents a KPI variant which is given in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes protease inhibitors that are analogues of the Kunitz protease inhibitor (KPI) domain of the amyloid precursor protein. The protease inhibitors can be used used to treat or prevent disorders associated with increased activity of serine proteases, specifically blood loss during surgery (particularly cardiopulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel enzyme inhibitors especially used to reduce postoperative bleeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin; amyloid precursor protein; coagulation factor; blood loss; cardiant; cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory; anti-arthritic; thrombolytic; antirheumatic; antipsoriatic; immunosuppressant; panoreatitis; deep vein thromboeis; psoriasis; rheumatoid arthritis; myocardial infarction; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                            Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrick BL,
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 3;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunitz protease inhibitor variant TW6182.
                                                                                                                                                                                                                                                                                         example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY68085 standard; protein; 61 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US012276.
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                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                            Sequence 61 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY68085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White RT,
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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                                                                                                                                                                                               The present invention relates to a method for modulating endothelial cell adhesion. The method comprises contacting an endothelial cell with a modulating peptide comprising a cadherin cell adhesion recognition sequence (His Ala Val) within a cyclic peptide ring. The method is useful for inhibiting angiogenesis, increasing vasopermeability, increasing blood flow to a tumour, disrupting neovasculature and inhibiting the development of endometriosis in a mammal. The modulating peptide reduces unwanted endothelial adhesion occurring between tumour cells, tumour cells and normal cells, normal cells as a result of surgery, injury, chemotherapy, disease and inflammation. The present sequence is one such
                                                                          Modulating endothelial cell adhesion for inhibiting development of endometriosis, increasing blood flow to tumor in a mammal, by contacting cell with a cyclic peptide having cadherin cell adhesion recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel enzyme inhibitors especially used to reduce postoperative bleeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin; amyloid precursor protein; coagulation factor; blood loss; cardiant; cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory; anti-arthritic; thrombolytic; anti-humatic; antipsoriatic; limmunosuppressant; pancreatitis; deep vain thrombosis; psoriasis; rheumatoid arthritis; myocardial infarction; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lucas AB
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          Ä
         Ali
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         Farookhi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY68110 standard; protein; 61 AA.
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                                                                                                                                                                  Claim 6; Page 64; 139pp; English.
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         Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
5; Conserv
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                                          WPI; 2002-049129/06
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                                                                                                                                                                                                                                                                                                                                                                               modulating peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8 AA;
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         Blaschuk OW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1999;
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Pollitt NS,
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Lucas AB;

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Gaps

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          durfaces in the heart-lung machine), but also other conditions such as pancreatitis; deep vain thrombosis; rheumatoid arthritis; psoriasis; myocardial infarction; and transplant rejection. They are also for organ preservation and to promote wound healing. In vitro the protease inhibitors are based on a human peptide cell extracts. The protease inhibitors are based on a human peptide sequence so are unlikely to be immunogenic, can be produced at high serine proteases. They are more potent or specific than known inhibitors. The present series proteases in they are more potent or specific than known inhibitors. The present sequence to present a kPI variant which is given in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, secreted protein, arthritis, Crohn's disease, sepsis, shock; ischaemia-reperfusion injury; haematopolesis, cancer; neuropathy; transgenic animal, Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis, bone degenerative disorder; thrombocytopenia; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
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T, Zhang J, Chen R, Xue AJ, Wang J;
bypass surgery where plasma proteases are activated by contact with
                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                            100.0%; Score 34; DB 3; Length 61; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secretory protein, Seg ID No 630.
                                                                                                                                                                                                                                                                                               Mismatches
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17-UUN-2000; 2000US-00596193.
14-UUL-2000; 2000US-00616847.
19-SEP-2000; 2000US-0066353.
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                                                                                                                                                                                                                                                                            Local Similarity 100.
1es 5; Conservative
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                           Sequence 61 AA;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU28273;
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The invention relates to novel isolated human secreted polypeptides (I) and (II) are useful for treating conditions such as arthritis, nephritis, Crohn's disease, inflammatory conditions such as arthritis, nephritis, Crohn's disease, inflammatory conditions such as arthritis, nephritis, Crohn's disease, and is increasing haematopolesis, stem cell survival, bone growth corphylaxis or treatment of one or more cancers (II) is also useful for prophylaxis or treatment of one or more cancers (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides.

(I) induces the proliferation of neural cells and respensention of nerve and brain tissue and is useful for the treatment of central and parintens disease, Huntington's disease, and amyoricophic lateral and parintens disease, Huntington's disease, and amyoricophic lateral and activity, regulation of haematopolesis and is useful for treatment of central and cretivity, regulation of haematopolesis and is useful for treating myeloid or lignorates, placelet disorders activity alsorders, placelet disorders activity and cell disorders, placelet disorders activity and or bone, cartilage, tendon, lignment and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcerangement of lung or liver fibrosis, or periodontal disease. Furthermore, (I) is also useful for gut procedion or regeneration and treatment of lung or liver fibrosis, creperfusion injury in various famunodeficiency (SCID), bacterial or the disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerossis, in addition, (I) affects blorbythms or circadian cycles of rhythms.

Creperfuse including severe combined immunodeficiency (SCID), bacterial or fundations, autoimmune disorders e.g. multiple sclerossis, in an antigence effects or other pale relations or circadian cycles of rhythms.

Creperfusers including severe co
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100.0%; Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid sequences of the invention
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99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
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Matches 5; Conserv
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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05-MAR-1999;
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9908-0144331P 9908-0144334P 9908-0144334P 9908-0144334P 9908-0144332P 9908-0144332P 9908-0144332P 9908-014432P 9908-014432P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014508P 9908-014638P 9908-014638P 9908-014638P 9908-014638P 9908-014932P 9908-014933P 9908-014932P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-014933P 9908-01508P 9908-015130P 9908-015130P 9908-015130P 9908-015130P	990S-0156458P- 990S-0156468P- 990S-0157117P- 990S-015713P- 990S-0157658P- 990S-015823P- 990S-0158369P-
19-70L-1999; 19-70L-1999; 19-70L-1999; 20-70L-1999; 21-70L-1999; 22-70L-1999; 23	24-SEF-1999; 29-SEF-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999; 07-OCT-1999; 08-OCT-1999;
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990S - 0127462P. 990S - 0128244P. 990S - 0128244P. 990S - 0120845P. 990S - 0120845P. 990S - 0130845P. 990S - 0130449P. 990S - 0130449P. 990S - 0132485P. 990S - 0134218P. 990S - 0134218P. 990S - 0134218P. 990S - 0134218P. 990S - 013425P. 990S - 013455P. 990S - 013455P. 990S - 0139455P. 990S - 0139453P. 990S - 0140353P. 990S - 0142055P.	90S-01 90S-01 90S-01 90S-01 90S-01 90S-01
01 - APR - 1999; 06 - APR - 1999; 07 - APR - 1999; 08 - APR - 1999; 08 - APR - 1999; 08 - APR - 1999; 09 - A	
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9908-013432P

9908-0139453P

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29-JUN-1999;
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        28-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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27-MAY-1999;
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1-700-1999;
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14-MAY-1999
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100.0%; Score 34; DB 3; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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9905-0123180P.
9905-0125788P.
9905-0125788P.
9905-0127462P.
9905-0127462P.
9905-0127462P.
9905-0129845P.
9905-013067P.
 990S-0159294P.
990S-0159294P.
990S-0159330P.
990S-0159330P.
990S-01596331P.
990S-0159634P.
990S-0160741P.
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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06-APR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                         100.0%; Score 34; DB 3; I
100.0%; Pred. No. 5.3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG38297 standard; protein; 244 AA
99US-0159638P.
99US-0159584P.
99US-0160741P.
99US-0160767P.
99US-0160814P.
99US-0160814P.
99US-0160819P.
99US-016088P.
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99US-0161404P.
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; Pred. No. 6.3e+02;
0; Mismatches 0; Indels
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PR 02-NUC-1999 9 90US-014538P.
PR 04-NUC-1999 9 90US-014538P.
PR 04-NUC-1999 9 90US-0147302P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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pharmaceutical.
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Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB74464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 58
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid molecule (I) encoding a Can 1 polypeptide. The Can 1 nucleic acid molecule is used to diagnose or treat infertility or premature ovarian failure or Sertoli Cell only syndrome in a mammal. The present sequence is that of the Drosophila melanogaster Can 1 protein of the invention. Note: The present sequence is not given in the printed specification but was obtained through the GenBank reference
                                                                                                                                                                                                                                                                                                                                            nucleic acid molecule (I) encoding a Can 1 polypeptide used in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin; virucide; antibacterial; anthrax; rhinovirus infection; common cold; intercellular adhesion molecule; ICAM-1; human; pig; porcine.
                                                                                                                        Human; Can 1; antiinfertility; gynaecological; infertility;
premature ovarian failure; menopause; Sertoli Cell only syndrome;
GenBank reference AAF54486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine intercellular adhesion molecule-1 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 5; Length 381; 100.0%; Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                         Drosophila melanogaster Can 1 SEQ ID NO 8.
                                              ABB83912 standard; protein; 381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE97396 standard; protein; 537 AA
                                                                                                                                                                                                                                                                                                       Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page; 45pp; English.
                                                                                                                                                                                                                          02-NOV-2001; 2001US-00003806
                                                                                                                                                                                                                                             03-NOV-2000; 2000US-0245872P
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Query Match
Best Local Similarity 100.v.
Best Local Similarity
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                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                      Bishop CE, Agoulnik AI,
                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                (BISH/) BISHOP C E. (AGOU/) AGOULNIK A I. (ZHUQ/) ZHU Q.
                                                                                                                                                                                                                                                                                                                          WPI; 2002-618953/66.
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318 CHAVC 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 381 AA;
                                                                                                                                                                                     US2002119929-A1.
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                                                                                     14-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                         infertility.
                                                                   ABB83912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE97396;
                                      ABB8391
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New immunoadhesin, useful for treating anthrax and rhinovirus, comprises chimeric toxin receptor protein linked to immunoglobulin heavy chain, and J chain and secretory component associated with the chimeric toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel immunoadhesin comprising a chimeric toxin receptor protein linked to at least a portion of an immunoadhesin heavy chain with a J (joining) chain and secretory component (SC) associated with the chimeric toxin receptor protein. The immunoadhesin comprises a chimeric bacterial or viral toxin receptor protein and the immunoadhesin has plant-specific glycosylation. The immunoadhesin of the invention demonstrates virucide and antibacterial activities and may be useful for reducing the binding of a viral or bacterial antigen to a host call and thus for treating or preventing anthrax, as well as human rhinovirus infection which results in the common cold. The current sequence is that of the porcine immunoadhesion-related protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-naturally occurring peptide; anion pump protein; tuberculosis; hypersensitivity reaction; tuberculostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae non-naturally occurring peptide #164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 74; 288pp; English.
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                                                                                                                                           (PLAN-) PLANET BIOTECHNOLOGY INC.
(LARR/) LARRICK J W.
(WYCO/) WYCOFF K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00311731.
25-OCT-2002; 2002WO-US034197
                                                                   26-OCT-2001; 2001US-00047542
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Best Local Similarity 100...
5; Conservative
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Query Match
Best Local Similarity
Matches 4; Conserv
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CHAIC 21
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                                                                                                                                                                                                               Sequence 75 AA;
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                                                                                                                                                                                                                           Mycobacterium tuberculosis comprising an amino acid sequence
Corresponding to an anion pump protein. The invention also relates to a
Corresponding to an anion pump protein. The invention also relates to a
Corresponding to an anion pump protein. The invention also relates to a
Corresponding to an anion pump protein. The invention also relates to a
Corresponding to acid corresponding to a DNA sequence of
Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is
Carioved from the sequence of the invention may elicit a specific immune
Corresponse. The peptide may also be used to detect hypersensitivity
Coractions of individuals exposed to Mycobacterium tuberculosis or
Mycobacterium leprae. The proteins and peptides may be affixed to solid
Cupponts to detect antibodies typical of hypersensitivity reactions, from
Corporation of individual peptide of the invention. Note: The sequence data for
Corporating peptide of the invention. Note: The sequence data for
Chis patent did not form part of the printed specification but was
Corporating electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia.
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                                                                                                                            New Mycobacterium tuberculosis anion pump peptide useful for tuberculosis vaccine and diagnosis of tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nanoarchaeum equitans cancer-associated (CA) protein #367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                           Disclosure; SEQ ID NO 213; 26pp; English.
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  (GENO-) GENOME THERAPEUTICS CORP
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                                                                                     WPI; 2003-656441/62
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nes 5; Conserv
                                             Mao J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 542 AA;
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                                          Smith DR,
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                                                                  The invention comprises then amino acid and coding sequences of cancerassociated (CA) genes isolated from Nanoarchaeum equitans. The invention also comprises the Nanoarchaeum equitans genome. The DNA and protein sequences of the invention are useful for diagnosing and treating cancer (e.g. carcinoma, lymphoma, or leukaemia). The present amino acid sequence represents a Nanoarchaeum equitans CA protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 8; Length 75;
Pred. No. 3.3e+02;
1; Mismatches 0; Indels
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, Jen S, Carter D;
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Claim 64; SEQ ID NO 735; 251pp; English.
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Propionibacterium acnes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequiate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maisonneuve JL;
Jones R, Carte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #11776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                  Score 33; DB 4; Length 176; Pred. No. 6.9e+02; 1; Mismatches 0; Indels
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 11776; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunostimulant; immune response; vaccine
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM47100 standard; protein; 176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
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                                                                                                                                                                                                                                  97.1%;
80.0%;
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                                                                                                                                                                                                                                                                          4; Conservative
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ing S, Jen S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
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                                                                                                                                                                                                                                                        Local Similarity
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CHAIC 57
                                                                                                                                                                                                                                                                                                               1 CHAVC 5
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                                                                                                                                                                                                Sequence 176 AA;
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patient. The P. acnes polypeptides, polynuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for disgnosaing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a disgnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                Score 33; DB 6; Length 176;
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                                                                                                                                                                                                                                                                                                                              Pred. No. 6.9e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herbicidally active polypeptide SEQ ID NO 1973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB92762 standard; protein; 428 AA.
                                                                                                                                                                                                                                                                                                                97.1%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                          Sequence 176 AA;
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Matches
       8566666666666655588
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97.1%; Score 33; DB 5; Length 428;

Query Match

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The present sequence is parvovirus non-structure protein 1 (NSI) variant (T463A). The invention relates to the variants of the parvovirus nonstructure protein (NSI) having a shifted equilibrium between the DNA replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                 NSI; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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                                                                                                                                                                                                                                                      /note= "Wild type Thr substituted with Ala"
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Pred. No. 2.1e+03;
1; Mismatches 0; Indels
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                                                                               Parvovirus non-structure protein 1 (NS1) variant (T463A)
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                                                                                                                                                                                                                        Location/Qualifiers
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(first entry)
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(first entry)
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Best Local Similarity 80...
4; Conservative
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N-PSDB; AAD02805.
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31-MAY-2001
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                               06-AUG-2003
31-MAY-2001
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 AAY72710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
                                                                                                                                                                                                                                                                                                                           NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy; tumoural disease; gene therapy; mutant; mutein; variant.
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80.0%; Pred. No. 2.1e+03;
ive 1; Mismatches 0; Indels
 Pred. No. 1.5e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          Parvovirus non-structure protein 1 (NS1) variant (T394A)
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                                                                                                                                                                      AAY72708 standard; protein; 672 AA
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80.08;
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(first entry)
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                   4; Conservative
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N-PSDB; AAD02803.
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Misc-difference 394
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Best Local Similarity
Matches 4; Conserv
Best Local Similarity
Matches 4; Conserv
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CHAIC 157
                                                   1 CHAVC 5
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31-MAY-2001
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Synthetic.
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Gaps

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RESULT 64 AAY72710 ID AAY7 XX

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The present sequence is a parvovirus wild-type non-structure protein 1 (NS1). The present invention relates to the variants of the parvovirus non-structure protein (NS1) having a shifted equilibrium between the DNA replication and transcription activities, and the cytoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
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                                                    Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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tumoural disease; gene therapy; mutant; mutein; variant.
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80.0%; Pred. No. 2.1e+03;
ive 1; Mismatches 0; Indels
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                                                                                                                               Disclosure, Fig 1, 41pp, English.
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(first entry)
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Best Local Similarity 80.0
Lag 4; Conservative
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WPI; 2001-212717/22.
N-PSDB; AAD02797.
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 CHAVC 5
                                                                                                                                                                                                                                                                                                                    Sequence 672 AA;
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31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                        Novel parvovirus non-structure protein variant, useful for treating tumoral diseases, has a shifted equilibrium between DNA replication and transcription activities, and cytotoxic activity.
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                                                      /note= "Wild type Thr substituted with Ala"
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Pred. No. 2.1e+03;
1; Mismatches 0; Indels
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                   Location/Qualifiers
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                                                                                                                                                                     99EP-00115161
                                                                                                                                                                                                          99EP-00115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00115161
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                                                                                                                                                                                                                                                                                 Rommelaere J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                      WPI; 2001-212717/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 CHAIC 382
                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD02801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 672 AA;
                     Key
Misc-difference
                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                          13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2003
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                                                                                          EP1077260-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2001.
                                                                                                                                 21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2001
                                                                                                                                                                                                                                                                                   Nueesch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nueesch J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY72702;
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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                    Peptide #2246 encoded by probe for measuring cervical gene expression.
                                                                                                                                                      human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #2315 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 31; DB 4; I
80.0%; Pred. No. 2.3e+02;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 20638; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR,
  AAM15812 standard; protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB34809 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-01801312P.
26-MAY-2000; 2000US-0207456F.
30-UJN-2000; 2000US-00601408.
03-AUG-2000; 2000US-006313166.
21-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-0234559P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000670
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                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                   cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAVC
                                                                                                                                                                                                                                                              WO200157278-A2
                                                                                                                                                                                                                        Homo sapiens.
                                                                               12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2002
                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB34809;
                                         AAM15812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                            Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 70
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ID ABB3
XC ABB:
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DE PEPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the human Colorectal Lesion Associated 2 (CLA2) gene (1; ADO34038), which is located on chromosome 5p14. CLA2 dequences are useful for the detection and treatment of proliferative disorders such as: a benign and malignant tumour (head, neck, respiratory tract, gastrointestinal tract, skin and its appendages, central and peripheral nervous system, arinary system, reproductive system, endocrine system, soft tissues and bone, lymphopoietic and haematopoietic system, breast, anogenital or colorectal cancers), a carcinoma or a dysplasia. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated colorectal lesion associated nucleic acid molecule useful in detection and therapy of proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome Sp14; proliferative disorder; tumour; cancer; carcinoma; dysplasia.
replication and transcription activities, and the cytotoxicity activity. These variants are useful as toxins for treating tumoural diseases. The variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                   Gaps
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                                                                                                                                       97.1%; Score 33; DB 4; Length 672;
80.0%; Pred. No. 2.1e+03;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%; Score 31; DB 8; Length 16;
80.0%; Pred. No. 1.9e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CLA2.3 peptide fragment, SEQ ID 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; SEQ ID NO 28; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                  ADO34065 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2002; 2002EP-00026772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-2002; 2002EP-00026772.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                        Best Local Similarity 80.0 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                                                                                                                                                                                                                             |||:|
CHAIC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MTMM-) MTM LAB AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHAVC 5
                                                                                                    Seguence 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-2004
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Best Local S
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                                                                                                                                                                                                                                                              378
                                                                                                                                                                                                                                                                                                                                                                                                         ADO34065;
                                                                                                                                         Query Match
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RESULT 6

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Length 20; 0; Indels Human; foetal liver; gene expression; single exon nucleic acid probe.

Homo sapiens

RESULT 69 AAM15812

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The invention relates to a spatially-addressable set of single exon
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                  human genetic disorders
                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                WPI; 2001-488897/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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CHALC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
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                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #2359 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 27444; 639pp + Sequence Listing; English
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM28322 standard; protein; 20 AA.
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26-MAY-2000; 2000US-0207456P.
30-UTM-2000; 2000US-00608408.
03-MUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                             03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%;
                                                                                              2001WO-US000669
                                                                                                                                      2000US-0180312P
                                                                                                                                                       26-MAY-2000; 2000US-0207456P
30-JUN-2000; 2000US-00608408
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                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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CHALC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 AA;
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                      WO200157277-A2
                                                                                              30-JAN-2001;
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                                                            09-AUG-2001
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                                                                                                                                                                           nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI3115-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #2282 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 4; Length 20;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 28591; 654pp; English.
                                                       DR;
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                                                           Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB29631 standard; peptide; 20 AA.
                                                                                                                                                                           Human genome-derived single exon r
gene expression in human placenta.
(MOLE-) MOLECULAR DYNAMICS INC
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                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000662
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2000US-00608408
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80.0%;
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increate acts proces to measuring years explained and a sample using the probes with a collection of detectably labelled nucleic acids derived probes with a collection of detectably labelled nucleic acids derived from manyly of human breast, and then measuring the label bound to each probe of the microarray. The probes useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring microarrays. The method is suitable for rapid sequence tag microarrays. The method is suitable for rapid sequence is a peptide nocoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO tells. It is the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein #2224 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
sample derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                   Length 20
                                                                                                                                                                                                                                                                                                                                                Score 31; DB 4;
Pred. No. 2.3e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; SEQ ID NO 21995; 530pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB20225 standard; protein; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-UJN-2000; 2000US-0060840B.
33-AUG-2000; 2000US-00632366.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       congenital heart disease.
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80..v
4, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI, 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHALC 5
                                                                                                                                                                                                                                                                                                                 Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 73
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probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, disgnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format disectly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 4; Length 20;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                     Length 20;
                                                                                                                                                                                       Score 31; DB 4; Length 20;
Pred. No. 2.3e+02;
1; Mismatches 0; Indele
                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                           AAM67996 standard; protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                       91.2%;
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                                                                                                                                                                                                                     4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microarray;
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Best Local
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Human liver peptide, SEQ ID No 28285.
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Best Local Similarity
Matches 4; Conserv
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                                                                    WO200157273-A2
                                                Homo sapiens.
                                                                                                                                 04-FEB-2000;
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                                                                                        09-AUG-2001
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ID AAM(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhaimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                          Human brain expressed single exon probe encoded protein SEQ ID NO: 27716.
                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR
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                                                                              AAM55611 standard; protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the probes of the invention
                                                                                                                       (first entry)
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Best Local Similarity
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         CHAVC 5
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                                                                                                                                                                                             Homo sapiens
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                                                                                                   AAM55611;
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ABG49637
ID ABG49
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AC ABG49
XX
DT 25-FE
XX
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe, human; breast disease, breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression in human adult liver.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000664
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2000US-00608408
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Chen W, Rank DR;

Hanzel DK,

2000US-00608408. 2000US-00632366. 2000US-0234687P.

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(MOLE-) MOLECULAR DYNAMICS INC
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                               30-JAN-2001; 2001WO-US000665
                                                                                       03-AUG-2000;
21-SEP-2000;
                                                                              30-JUN-2000;
           15-NOV-2001
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                                                                                                                                                                                                                                                                                         The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fib. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                 Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide encoded by genome-derived single exon probe SEQ ID 27193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromacrosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary hatclocytosis; lymphangiolejomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cillary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 4; Length 20;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 12290; 322pp; English.
                                                                                                                                                                                      Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG37528 standard; peptide; 20 AA
                                                                             26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-02346BPP.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
                                                                   2000US-0180312P
                                             29-JAN-2001; 2001WO-US000661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK,
                                                                                                                                                                                                           WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 AA;
WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                    04-FEB-2000;
                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG37528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG37528
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Complements relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of the first nucleic acid sequences mentioned in the specification, or their complements or the 1239 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic cid expressed in the human lung; measuring gene expression in a sample cit the novel set of probes which hybridise acids derived from human lung; omprising on contacting the array with a sample collection of detectably labeled nucleic acids derived from human lung comprising of a collection of detectably labeled nucleic acids derived from human lung array; identifying at least one exon from genomic sequences of the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting a predicting a predicting at least one comprising (a) array; identifying a fragment identical to the predicted exon, the probe; is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and/or cell types using hybridisation to a single exon in several tissues and/or cell types using hybridisation to a single exon for comprising one the exons should be assigned to a single gene; a peptide comprising one comprising of the exons should be assigned to a single gene; a peptide comprising compression of the exons multioned in the specification, or encoded by the corposycen manybais, and for identifying exons in a gene particularly warm and for identifying exons in a gene particularly using human analysis, and for identifying exons in a gene particularly using human analysis, and for identifying exons in a gene particularly using human analysis, and for identifying exons in the probes particularly are publicated mRNA and for the study of lung d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
                                                                              Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon
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                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 27193; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
WPI; 2002-114183/15
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Page

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Gaps

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Indels

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Mismatches

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in the specification) describes subscultanty putnitude interest to as open reading frame. ORFX, where X is 1-11491 (see Table In the specification). ABN15762 to ABN27252 encode the human ORFX proteins are useful for reating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders infectious transplantation, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, ulcers, myasthenia gravis, graft-versus-host contection or regeneration and treatment of lung or liver fibrosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from reperfusion injury in various tissues and conditions resulting from reperfusion injury in various tissues and conditions resulting from reperfusion injury in various, but was obtained in electronic form part of the princed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypethyoidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autolmmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 15026; 1037pp; English.
                                                                                                                                                                                         Human ORFX protein sequence SEQ ID NO:15026.
                                             ABP07522 standard; protein; 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                            myasthenia gravis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                            24-JUN-2002
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                                                                                            ABP07522;
RESULT 79
                         ABP07522
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Length 53;

Score 31; DB 5; Pred. No. 5.1e+02;

91.2%; 80.0%;

Query Match Best Local Similarity

Sequence 53 AA;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostic responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and can sequences. ABG00010-ABG30377 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                       forensic;
                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic. food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 39191; 103pp; English.
                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #8823.
                                                                                                                                                                                              ABG08832 standard; protein; 58 AA.
  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                 (first entry)
4; Conservative
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Matches 4; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                   27 CHSVC 31
                                           1 CHAVC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                    13-FEB-2002
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                                                                                                                                                                                                                                         ABG08832;
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  Matches
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(first entry)

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphom; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obsety; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human secreted proteins and coding sequences useful for treating disorders of the immune system and hyperproliferative disorders.
                                         Human secreted protein encoded by gene No. 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 381; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-337740/28.
N-PSDB; AAX84986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feng P, Carter F
Ni J, Wei Y, Mc
Shi Y, Ebner R;
                                                                                                                                                                                                           Homo sapiens
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07-NOV-1997;
17-NOV-1997;
               30-JUL-1999
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07-NOV-1997
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 The invention relates to human polynuclectides (AAI79941-AAI91841) and the encoded proteins (AA000010-AA019910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokine, or other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 20; SEQ ID NO 23550; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.2%; Score 31; DB 4; Length 61;
80.0%; Pred. No. 5.8e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                             Human polypeptide SEQ ID NO 23550.
                                                                                                       AAO09658 standard; protein; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                 (first entry)
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Best Local Similarity 80.v.
--- 4; Conservative
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N-PSDB; AAI89589.
CHAVC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                 WO200164835-A2.
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                 06-NOV-2001
                                                                                                                                     AAO09658;
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97US-0064900P.
97US-0064911P.
97US-0064911P.
97US-0064912P.
97US-0064913P.
97US-0064918P.
97US-0064918P.
97US-0064918P.
97US-0066918P.
97US-0066090P.
97US-0066090P.

98WO-US023435

ir KC, Endress GA, Rosen CA, Ruben SM, Janat F; Moore PA, Soppet DR, Kyaw H, Lafleur DW, Olsen HS;

Carter KC,

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This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX84924) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 125 novel genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino acid sequences AAX75567-X7933) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the expressed in (see AAX84933 for described uses)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.2%; Score 31; DB 2; Le:
80.0%; Pred. No. 5.9e+02;
ive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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Gaps

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AAY27620 standard; protein; 63 AA.

RESULT 82 AAY27620 ID AAY2 XX AC AAY2

AAY27620

||:|| 53 CHSVC 57

1 CHAVC 5

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formatirectly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #1634 encoded by probe for measuring placental gene expression.
                                   Human; foetal liver; gene expression; single exon nucleic acid probe.
Peptide #1640 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 26769; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 4; Length 63;
Pred. No. 5.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM27597 standard; protein; 63 AA.
                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                           2000US-0207456P.
2000US-00608408.
2000US-00632366.
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                                                                                                                                                                                      30-JAN-2001; 2001WO-US000669.
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27-SEP-2000; 2000US-0236359P
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                                                                                                                                                                                                                                                                                                                                        04-OCT-2000; 2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
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36 CHALC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157272-A2
                                                                                                            WO200157277-A2
                                                                                                                                                                                                                                           26-MAY-2000; 30-JUN-2000; 203-AUG-2000; 20
                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                           04-FEB-2000;
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                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM27597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                          Peptide #1576 encoded by probe for measuring cervical gene expression.
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                                                                                                                                                                                                                                               Probe; human; microarray; gene expression; cervical epithelial cell;
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Pred. No. 5.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 19968; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB34134 standard; peptide; 63 AA.
                                                                                             AAM15142 standard; protein; 63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%;
80.0%;
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21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0235359.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207456P.
                                                                                                                                                                     12-OCT-2001 (first entry)
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CHALC 40
 CHSVC 23
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                                                                                                                                                                                                                                                                  cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63 AA;
                                                                                                                                                                                                                                                                                                                                          WO200157278-A2
                                                                                                                                                                                                                                                                                                       Homo sapiens
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 13
                                                                                                                                  AAM15142;
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Best Local S
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ABB34134
                                                        RESULT 83
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from which a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes are useful for verifying the care useful for gene discovery, and for determining predisposition and/or proposing breast disease. Gene expression analysis is useful for sassessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring cases expression, with far less bias than expressed sequence tag microarrays. The method is suitable for repaid production of functional information from genomic sequence. The present sequence is a peptide ancomic acid probe of the invention. Note: The sequence date for this patent did not form part of the printed sequences.

Sequence date for this patent did net form part of the printed sequences.

Sequence date for this patent did net form part of the printed sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein #1574 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human hearts.
                            Claim 27; SEQ ID NO 11934; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, gene expression, heart, microarray, vascular system;
cardiovascular disease, hypertension, cardiac arrhythmia,
comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 4; Pred. No. 5.9e+02; 1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB19575 standard; protein; 63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053256.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023599P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                               91.2%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                 Sequence 63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CHAVC
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                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 63;
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                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 27866; 654pp; English.
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                                                                                                                                     Rank DR
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                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                      Chen W,
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
                 30-JUN-2000; 2000US-00608408.
03-MG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02353599.
04-OCT-2000; 2000GB-00024263.
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27-SEP-2000; 2000US-0236359P
04-OCT-2000; 2000GB-00024263.
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80.0%;
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    2000US-0207456P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80...
4; Conservative
                                                                                                                                     Penn SG, Hanzel DK,
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                                                                                                                                                                 WPI; 2001-488897/53
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36 CHALC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer.
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Gaps

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Length 63; 0; Indels

Thu Jul

Sequence 63 AA;

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                                             measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                Gaps
                                  present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO: 27611.
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                                                                                                                                                                                                                                                                                          91.2%; Score 31; DB 4; Length 63;
80.0%; Pred. No. 5.9e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Length 63;
                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
Claim 15; SEQ ID NO 21345; 530pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM67305 standard; protein; 63 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456P
30-JUN-2000; 2000US-0060840B
03-AUG-2000; 2000US-00632366
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                                                                                                                                                                                                                                                                                                            Local Similarity 80.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                    36 CHALC 40
                                                                                                                                                                                                                                                                                                                                                                1 CHAVC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                Human, brain expressed exon, gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                      Human brain expressed single exon probe encoded protein SEQ ID NO: 27029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid
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Pred. No. 5.9e+02;
; Mismatches 0; Indels
Score 31; DB 4; Length 63;
Pred. No. 5.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                       AAM54924 standard; protein; 63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK, Chen W,
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 91.2%;
80.0%;
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04-OCT-2000; 2000GB-00024263.
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03-AUG-2000; 2000US-00632366
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21-SEP-2000; 2000US-0234687P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the probes of the invention
                                                                                                                                                                                                           (first entry)
                              4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483446/52.
 Query Match
Best Local Similarity
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Best Local Similarity
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36 CHALC 40
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                                                        1 CHAVC 5
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                                                                                                                                                                                                                                                                                                                                     WO200157275-A2
                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                 Best Loc
Matches
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                                                                                요
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ABG48967 standard, peptide; 63 AA.

ABG48967 ID ABG4

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1 CHAVC
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                                                WO200157270-A2
                             Homo sapiens.
                                                                                       29-JAN-2001;
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27-SEP-2000;
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                                                                                                                                            03-AUG-2000;
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                                                                     09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in nolved in genetic liver diseases such as cirrhosis, hyperlippoproceinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG4734-ABG59930 represent human liver mingle exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the whop.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #1565 encoded by probe for measuring breast gene expression.
                                                                  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 31; DB 4; Length 63; 80.0%; Pred. No. 5.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 27615; 658pp; English
                                                                                                                                                                                                                                                                                          Rank DR
                                                 Human liver peptide, SEQ ID No 27615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM02883 standard; protein; 63 AA
                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                              26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
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                               (first entry)
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Best Local Similarity 80.0°
                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                               WPI; 2001-488898/53
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36 CHALC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHAVC 5
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                                                                                                                        WO200157273-A2
                                                                                                     Ното варіеля
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           ABG48967;
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The present invention relates to novel single exon nucleic acid probes (see AAIO0010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast diseases and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
       Probe, human, breast disease, breast cancer, development disorder;
inflammatory disease, proliferative breast disease, non-carcinoma tumour.
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development disorder;
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80.0%; Pred. No. 5.9e+02;
tive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312P.
2000US-0207456P.
2000US-0608408.
2000US-023366.
2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476286/51
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36 CHALC 40

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RESULT 93

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CHAVC

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present sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                              Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 26617; 634pp; English.
                                                                                                                                                                            Rank DR;
                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                            Chen W,
                                                                                                               03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235359
04-OCT-2000; 2000GB-00024263.
                                                                     30-JAN-2001; 2001WO-US000665
                                                                                      2000US-0180312P
                                                                                                26-MAY-2000; 2000US-0207456P
30-JUN-2000; 2000US-00608408
hyaline membrane disease
                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                              WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63 AA;
                                   WO200186003-A2
                 Homo sapiens
                                                                                      04-FEB-2000;
                                                    15-NOV-2001
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Claim 20; Page 1089; 1275pp; English.
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               AAM24070 standard; protein; 85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-0061746.
03-MUG-2000; 2000US-00651451.
15-SEP-2000; 2000US-00663870.
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80.0%;
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                                                                                                 (first entry)
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N-PSDB; AAH98729.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 85 AA;
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                                                                                                                                                                                                                                                                                                                                       WO200154477-A2
                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                    12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001.
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                                                         AAM24070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 94
AAU14419
ID AAU14.
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AC AAU14.
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AAM24070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring the array with a carid expressed in the human lung; measuring the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contracting the array with a collection of detectably labeled nucleic acids derived from human lung array; identifying exons in a elwaryotic genome, comprising (a) adentifying exons in a elwaryotic genome, comprising (b) adetecting at least one exon from genomic osquences of the array is a fragment identical to the predicted exon, the probe is included in the above mentioned microarray sesigning exons to a single exon probe, and (b) measuring the expression of each of the exons in several crossing (a) identifying exons from genomic sequence by the method above mentioned microarray assigning exons to a single exon in the above mentioned microarray and/or call types using hybridisation to a single exon in croarrays having a probe with the exon, where a common pattern of expression of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression cancer, chronic obstructive pulmonary fibrosis, or encoded by the crome pattern of desesse (IDD), farming a language exon in a gene, particularly using human cuberous sclerosis, gaucher's disease, pulmonary disease (COPD), interstitial lung cancer, chronic obstructive pulmonary places, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.2%; Score 31; DB 5; Length 63;
80.0%; Pred. No. 5.9e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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                                                     Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YT, Liu C, Zhou P, Qian XB, Wang
?, Drmanac RA, Zhang J, Werhman T;
Human EST encoded protein SEQ ID NO: 1595.
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ADH80737 standard; protein; 96 AA.

ADH80737;

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Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; antiaconvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antialiergic; dermatological; hamostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                       Isolated polypeptides useful for treating anti-inflammatory diseases,
nervous system disorders, and for regenerating bone and cartilage.
                                                                                                                                                                                                                                                                                                                                       Example 4; Page 808; 894pp; English.
                                                                                                                                                                                                                                                      Drmanac RT;
                                                                                                                                                                                         25-JAN-2001; 2001WO-US002623
                                                                                                                                                                                                            25-JAN-2000; 2000US-00491404
24-OCT-2001 (first entry)
                     Human novel protein #290
                                                                                                                                                                                                                                                                          WPI; 2001-451939/48.
                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                     N-PSDB; AAS22724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96 AA;
                                                                                                                                               WO200155437-A2
                                                                                                                            Homo sapiens.
                                                                                                                                                                    02-AUG-2001
                                                                                                                                                                                                                                                     Tang YT,
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies craised against the polypeptides, polynucleotides and antibodies are massed an amethod of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight expression or activity. The polypeptides can be used as molecular weight are used to identify compounds which bind to the polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of tecombinant proteins, and in generating anti-sense DNA or RNA and in generating plodies/elicit an immune response, to determine duantitative protein levels, as tissue markers, and to isolate receptors or ligands. Solypeptides of the invention may also be useful in treating platelet disorders, regenerating bourne, tendon, alignment and/or nerve tissue, wound healing, treating burne, promoting the proliferation, differentiation and survival of stem calls, as a manner and the proliferation and survival of stem calls. contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system diseachers, and infection. The present sequence represents a protein of the invention

Gaps ; Score 31; DB 4; Length 96; Pred. No. 8.5e+02; 1; Mismatches 0; Indels 91.2%; 80.0%; 4; Conservative Query Match Best Local Similarity Matches

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CHAVC 5 -

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CHSVC 85 81 ö

Gape

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Length 96; 0; Indels

Score 31; DB 8; I Pred. No. 8.5e+02; 1; Mismatches 0;

91.2%; 80.0%;

Query Match Best Local Similarity

4; Conservative

Matches

1 CHAVC 5

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RESULT 95
ADH80737
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The invention relates to new isolated polynucleotides and polypeptides. The sequences, compositions and methods of the invantion are useful for diagnosimy, preventing or treating diseases involving aberrant protein expression or biological activity, such as cosquiation disorders (e.g. haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer, bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune disorders. The polynucleotides may be used as hybridisation probes, as oligoners or primers, for polymerase chain reaction, for chromosome and gene mapping, in the recombinant production of proteins and in generation antibodies, as molecular weight markers or as food supplements. This sequence represents a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and polypeptides useful for diagnosing, preventing or treating diseases involving aberrant protein expression or activity, e.g. hemophilis, wounds, stroke, thrombosis, cancer or autoimmune disorders.
                                                                                                            Human, coagulation disorder, haemophilia, wound, stroke; thrombosis; myocardial infarction; cancer; bone fracture; Alzheimer's disease; barkinson's disease; autoimmune disorder; food supplement; haemostatic; vulnerary; cerebroprotective; thrombolytic; anticoagulant; cardiant; cytostatic; osteopathic; neuroprotective; nootropic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB, Wang ZW, Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 762; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen R,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                            2000US-00617746.
2000US-00631451.
2000US-00663870.
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03-AUG-2001; 2001US-00922279
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                                                        (first entry)
                                                                                  Human polypeptide #54
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ZHANG J.
ZHOU P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LIU C.
ASUNDI V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRMANAC R
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QIAN X B
WANG Z W
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                                                                                                                                                                                                                  Homo sapiens.
                                                       22-APR-2004
                                                                                                                                                                                                                                                                                                                                25-JAN-2000;
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(WANG/)
(WEHR/)
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(ZHOU/)
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(ASUN/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                 (TANG/)
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ADO34044 ID ADO RESULT

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Sato H, Ishii S;
K, Irie R, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel human polynuclectide and the encoded polypeptide. A polynuclectide of the invention may have a use in gene therapy. An oligonuclectide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynuclectide or as a probe for detecting the polynuclectide. The polynuclectides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynuclectides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                           Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3908; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #5981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG05990 standard; protein; 134 AA.
                                                                                                                                                                        (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                               12-APR-2002; 2002EP-00008400.
                                                                                                                                22-MAR-2002; 2002JP-00137785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                          T, Sugiyama T, o J, Isono Y, H
                                                                                                                                                                                                                                                                                       2003-723558/69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                           N-PSDB; ADM02780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
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                     EP1347046-A1
                                                                                                                                                                                                                               Yamamoto J,
                                                           24-SEP-2003.
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                                                                                                                                                                                                                                                 Seki N,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated colorectal lesion associated nucleic acid molecule useful in the detection and therapy of proliferative disorders.
                                                                                                                                                                                                                                                                     Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome 5p14; proliferative disorder; tumour; cancer; carcinoma; dysplasia.
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80.0%; Pred. No. 8.8e+02;
cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein of the invention SEQ ID NO:3908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 7; 123pp; English
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                                                                                                                ADO34044 standard; protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2002; 2002EP-00026772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-2002; 2002EP-00026772.
                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                               Human CLA2.3, SEQ ID 7.
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CHSVC 85
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                                                                                                                                                        ADO34044;
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                     81
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Best Loc Matches

RESULT 97

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ADMO5223
ID ADMO
XX AC ADMO
XX DDT 20-N
DT 20-N
DE Hume
XX Hume
OS HOMO

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Gaps

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2003-748383/70.
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                      N-PSDB; ADM27081
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Chen J;
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                                                                                                                              The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from MIPO at
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                                               New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels
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                                                                                                            Claim 20; SEQ ID NO 36349; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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16-SEP-2002; 2002US-0410974P.
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            WPI; 2001-639362/73.
N-PSDB; AAS70177.
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Best Local Similarity
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                                                                                                                                                                                                The invention comprises the amino acid sequence of proteins from the hyperthermophile Methanopyrus kandleri, the invention also comprises the complete genome from Methanopyrus kandleri. The Methanopyrus kandleri aproteins of the invention are useful for enhancing the stability and/or activity of other proteins. The Methanopyrus kandleri genome is useful in a variety of diagnostic and analytical methods. The present amino acid sequence represents a Methanopyrus kandleri protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, vaccine, exbB receptor antagonist, tumour, cancer, gastric cancer,
breast cancer, prostate cancer, exbB receptor subdomain IV.
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New isolated nucleic acids encoding any of about 1700 Methanopyrus kandleri proteins, and the encoded proteins, useful as a medicaments or as diagnostic agents.
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80.0%; Pred. No. 1.2e+03;
ive 1; Mismatches 0;
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                                                                                                                                          Claim 31; SEQ ID NO 903; 1023pp; English.
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03-AUG-2001; 2001US-0309864P.
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Query Match 91.2%; Score 31; DB 6; Length 148; Best Local Similarity 80.0%; Pred. No. 1.2e+03; Matches 4; Conservative 1; Mismatches 0; Indels
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Search completed: July 26, 2005, 23:58:04 Job time : 168 secs

93, Appl 96, Appl 96, Appl 96, Appl 96, Appl 96, Appl 101, Appl 1016, A

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US-09-347-88-912-80
US-09-348-455-82
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9.104 Million cell updates/sec
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/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-50-102-8

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US-09-248-074-10

US-09-458-870-10

US-09-057-363C-22

US-09-057-363C-22

US-09-057-363C-34

US-09-057-363C-34

US-09-057-363C-34

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5.09-458-870-84

5.09-458-870-87

5.09-458-870-91

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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Result Š 111, Appl 15175, Appl 10177, Appl 10986, Appl 10986, Appl 10986, Appl 52, Appl 2, Appl 2, Appl 12, Appl 12, Appl 2, Appl 2, Appl 118, Appl 2, Appl 3, Appl 3, Appl 3, Appl 3, Appl 4, Appl 4, Appl 6, Appl 6, Appl 7, Appl 8, Appl 8,

454, App 35, Appl 35, Appl 35, Appl 7139, Ap 39899, Ap 55116, A

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Query Match 100.0%; Score 34; DB 3; Length 5; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 5; Conservative 0; Mismatches 0; Indels
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,679
FILING DATE: 33-DEC-1997
CCLASSIFICATION NUMBER: 31.392
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 100086.401C1
FELEPHONE: (206) 622-6031
FELEPHONE: (206) 622-6031
FILEFAX: (206) 62-6031
FILEFAX: SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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US-09-115-395-10
Sequence 10, Application US/09115395A
; Patent No. 6207639
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CHAVC 5
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                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: GOUV. Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING TITLE OF INVENTION: CELL ADHESION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRAFE: Washington
COUNTRY: USA
ZIP: 98104
COUNTRY: USA
ZIP: 98104
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATCATION DATA:
APPLICATION NUMBER: US/08/893,534A
FILING DATE: 11-JUL-1997
CLASSIFICATION NUMBER: 330
ATTORNEY/AGENT INFORMATION:
NAME: MARAL, DAVIG J.
REFERENCE/DOCKET NUMBER: 100086.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELECOMMUNICATION NUMBER: 31,392
REFERENCE CHARACTERISTICS:
LENGTH: S maino acide
TVDF: Amino acide
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| Patent No. 6169071 |
| GENERAL INFORMATION: |
| APPLICANT: Blaschuk, Orest W. |
| APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING |
| TITLE OF INVENTION: CELL ADHESION |
| TITLE OF INVENTION: CELL ADHESION |
| TITLE OF INVENTION: CELL ADHESION |
| TITLE OF SEQUENCES: 63 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: SEED and BERRY LLP |
| STREET: 6300 Columbia Center, 701 Fifth Avenue |
| CITY: Seattle |
| STATE: Washington |
| COUNTRY: USA |
| COUNTRY: USA |
| COUNTRY: USA |
| COUNTRY: USA |
| COUNTRY: CALL |
| COUNTRY: USA |
| COUNTRY: CALL |
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                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                 US-08-893-534A-8
Sequence 8, Application US/08893534A
Patent No. 6031072
GENERAL INFORMATION
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
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CHAVC 5
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ZIP: 98104
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US-08-996-679-8
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Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Solid Phase

OTHER INFORMATION: Synthesis
US-09-115-395-10
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US-09-507-102-8

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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-248-074-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BLASCAUK, Orest W.
APPLICANT: BLASCAUK, Orest W.
APPLICANT: Gour, Barbara J.
TILE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION FILE REFERENCE: 100086.4016.5
CURRENT APPLICATION NUMBER: US/09/248,074
CURRENT FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 10
LENGTH: 5
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide Cycler INFORMATION: with Classical Cell Adhesion Recognition Sequence; PEATURE: OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-250-059-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORNATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Barbara J.
APPLICANT: Farookhi, Darbara J.
APPLICANT: Farookhi, Darbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY FILE REFERENCE: 100086.401C7
CURRENT APPLICATION NUMBER: US/09/357,717
CURRENT FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                      Length 5;
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100.0%; Pred. No. 4.1e+05;
tive 0; Mismatches 0;
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; Sequence 10, Application US/09357717
; Patent No. 6417325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-248-074-10; Sequence 10, Application US/09248074; Sequence 10, Application US/09248074; Patent No. 6346512; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
5, Conserve
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LENGTH: 5
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US-09-250-059-10
Sequence 10, Application US/09250059
Patent No. 6333307
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
FILE REFRENCE: 100086.401.C6
CURRENT APPLICATION NUMBER: US/09/250,059
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 10
LENGTH: 5
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              Sequence o, heres
Patent No. 6326352
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
Gour, Barbara J.
TITLE OF INVENTION: CELL ADHESION
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED IP LAW GROUP PLLC
STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READMED FORM:

COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,102
FILING DATE: 17-Feb-2000
CLASSIFCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,534
FILING DATE: 11-JUL-1996
FILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.401C10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
            Sequence 8, Application US/09507102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5 amino acids
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                 STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                             CITY: Seattle
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Best Local Similarity
Matches 5; Conserval
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APPLICANT: Blaschuk, Orest W.
Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC COMPATIONS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: VINKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: CLASSIFICATION NUMBER: 44,614
REGISTRATION NUMBER: 44,614
RECOMMUNICATION INFORMATION:
TELEFAK: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 4; L
100.0%; Pred. No. 4.1e+05;
ive 0; Mismatches 0;
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REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-057-363C-34; Sequence 34, Application US/09057363C; Patent No. 6551994; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 5 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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US-09-057-363C-22
i Sequence 22, Application US/09057363C
; Sequence 22, Application US/09057363C
; Patent No. 6551994
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
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US-09-458-870-10
i Sequence 10, Application US/09458870
j Patent No. 6465427
j GENERAL INFORMATION:
j APPLICANT: Blaschuk, Orest W.
j APPLICANT: Gour, Barbara J.
j APPLICANT: Ali, Anmar
j TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
j TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
j CURRENT APPLICATION NUMBER: US/09/458,870
j CURRENT APPLICATION NUMBER: US/09/458,870
j CURRENT PILING DATE: 1999-12-10
j SOFTWARE: Patentin Ver. 2.0
j SEQ ID NO 10
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence FEATURE:
            OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
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                                                                              Cyclic Peptide may comprise N-terminal modification such as acetyl or alkoxybenzyl group and/or C-terminal modifications such as amide or
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ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104
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                                                                                 OTHER INFORMATION: Cyclic Pepti
OTHER INFORMATION: modification
OTHER INFORMATION: and/or C-ter
OTHER INFORMATION: ester group
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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CHAVC 5
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Sequence 296, Application US/09234395 Patent No. 6680175
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; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-296
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               OTHER INFORMATION: ester group
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ORGANISM: Artificial Sequence
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US-09-305-928-296
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US-09-234-395-296
                     ; OTHER INFORM
US-09-544-782-10
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APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Area Gour, Barbara J.
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION FILE REFERENCE: 100086.401C9
CURRENT APPLICANTION NUMBER: US/09/544,782
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 10
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
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                                                                                                           Gapa
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                                                                   100.0%; Score 34; DB 4; Length 5; 100.0%; Pred. No. 4.1e+05; tive. 0; Mismatches 0; Indels
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-057-363C-34
                                                                                                                                                                                                                                       RESULT 11
18-09-248-015-10
1 Sequence 10, Application US/09248015
2 Patent No. 6562786
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                                                                     Query Match
Best Local Similarity 100.09
Matches 5; Conservative.
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Best Local Similarity 100.
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OTHER INFORMATION: Description of Artificial Sequence: Product of OTHER INFORMATION: Synthesis and Cyclization based on Human OTHER INFORMATION: N-Cadherin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Byers, Stephen
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
FILE REFERENCE: 100066.40 TG
CURRENT APPLICATION NUMBER: US/09/305,928
CURRENT FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 296
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APPLICANT: Blaschuk, Orest W.

APPLICANT: Byers, Stephen

APPLICANT: Byers, Stephen

APPLICANT: Gores, Stephen

TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER

TITLE REFERENCE: 100086.40702

CURRENT APPLICATION NUMBER: US/09/234,395

CURRENT FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 324

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 296

LENGTH: 5
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Length 5;
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                             4.1e+05;
  100.0%; Score 34; DB 4;
100.0%; Pred. No. 4.1e+05
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Sequence 10, Application US/10058821
Patent No. 6780845
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                  Sequence 22, Application US/09265107A

Sequence 22, Application US/09265107A

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: GENE EXPRESSION AND CELLULAR DIFFERENTIATION

FILE REFERENCE: 100086.406C1

CURRENT APPLICATION NUMBER: US/09/265,107A

CURRENT PILING DATE: 1999-03-09

NUMBER OF SEQ ID NOS: 75

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 22

LENGTH: 5
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Sequence 34, Application US/09265107A
Setent No. 6693048
GENERAL INFORMATION;
APPLICANT: Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR STIMULATING
TITLE OF INVENTION: GENE EXPRESSION AND CELLULAR DIFFERENTIATION
FILE REFERENCE: 100086.406C1
CURRENT FILING DATE: 1999-03-09
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 3.0
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 100.0%; Score 34; DB 4; Length 5; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
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US-09-265-107-22
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100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0;
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Matches 5; Conservative
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US-09-265-107-22
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RESULT 17

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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Riaz
APPLICANT: Barbara J.
APPLICANT: Barbara J.
APPLICANT: Barbara J.
APPLICANT: Barbara J.
TITLE OP INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
FILE REFERENCE: 100086.401C12
CURRENT APPLICATION NUMBER: US/10/058,821
CURRENT FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 58
SOFTWARE: ParentIN Ver. 2.0
SOFTWARE: ParentIN MAINTION: MODIFICATION SUCH AS ARICH OF THE INFORMATION: ester group
SOFTWARE: ParentIN SOFTWARE: SOFTWARE
SOFTWARE: ParentIN SOFTWARE
SOFTWARE
SOFTWARE: ParentIN SOFTWARE
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Sequence 64 Application US/09458870

Jacent No. 6465427

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Blaschuk, Riaz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

TITLE OF INVENTION COMPOUNDS.

CURRENT APPLICATION NUMBER: US/09/458,870

CURRENT APPLICATION NUMBER: US/09/458,870

WUMBER OF SEQ ID NOS: 101

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
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Sequence 92, Application US/09458870

Setent NO. 6465427

GENERAL INFORMATION:
APPLICANT: Blaschurk, Orest W.
APPLICANT: Blaschurk, Orest W.
APPLICANT: Brockhi, Riaz
APPLICANT: Farockhi, Riaz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TITLE OF FILING DATE: 1999-12-10
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                APPLICANT: Blaschuk, Orest W.
APPLICANT: Barbara J.
APPLICANT: Barbara J.
APPLICANT: Farcockhi, Riaz
APPLICANT: Farcockhi, Riaz
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REPERENCE: 100086.401C8
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: Cyclic Peptide with Classical Cell Adhesion Recognition Sequence
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100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                 US-09-458-870-91
; Sequence 91, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity luv.
5, Conservative
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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; Sequence 88, Application US/09458870
; Ratent No. 6465427
; GENERAL INFORMATION;
APPLICANT: Blachuk, Orest W.
; APPLICANT: Farochhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT PILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
                                      Sequence 87, Application US/09458870

Patent No. 6465427

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Parcokhi, Riaz

APPLICANT: Ali, Annar

TITLE OF INVERTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

FILE REFERENCE: 100086.401C8

CURRENT APPLICATION NUMBER: US/09/458,870

CURRENT FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PATENTIN Ver. 2.0
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5, Conservative
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US-09-458-870-88
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                           US-09-458-870-87
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; Sequence 84, Application US/09544782; Patent No. 6610821; GENERAL INFORMATION:
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Patent No. 6610821
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Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-09-544-782-84
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                                                                                                                                                                                                                                                                    APPLICANT: BLASCHUK, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: ATI, Amar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 93
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APPLICANT: Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Garockhi, Riaz
APPLICANT: Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 100
LENGTH: 6
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-09-458-870-100
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                                                                                                                                                                                              Sequence 93, Application US/09458870; Patent No. 6465427; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Farcockii, Riaz
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401C9
CURRENT APPLICATION NUMBER: US/09/544,782
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Riaz
APPLICANT: Farcockhi, Riaz
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REPERENCE: 100086.40109
CURRENT APPLICATION NUMBER: US/09/544,782
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: ester group
US-09-544-782-54
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      Length 6;
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100.0%; Score 34; DB 4; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0;
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; Sequence 91, Application US/09544782; Patent No. 6610821
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-09-544-782-88
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; Sequence 88, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TILLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 88
LENGTH: 6
                                                                                                                                                                                                                                    Sequence 87, Application US/09544782
; Sequence 87, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFRENCE: 100086.40107
; FILE REFRENCE: 100086.40107
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 87
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                                                               Gaps
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  100.0%; Score 34; DB 4; Length b; 100.0%; Pred. No. 4.1e+05; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
                  Query Match 100.
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Matches 5; Conservative
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US-09-544-782-87
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Sequence 92, Application US/09544782

Sequence 92, Application US/09544782

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Farookhi, Riaz

APPLICANT: Farookhi, Riaz

APPLICANT: Farookhi, Riaz

TILLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

FILE REFERENCE: 100086.401C9

CURRENT FILING DATE: 2000-04-07

CURRENT PILING DATE: 2000-04-07

SEQ ID NOS: 96

SEQ ID NOS: 96

SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blaachuk, Orest W. APPLICANT: Blaachuk, Orest W. APPLICANT: Gour, Barbara J. APPLICANT: Gour, Barbara J. APPLICANT: Farockhi, Riaz APPLICANT: Ali, Anmar TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION FILE REFERENCE: 100086.401C9 CURRENT APPLICATION NUMBER: US/09/544,782 CURRENT FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 96 SOFTWARE PATENTIN Ver. 2.0 SEC ID NO 91 LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
CTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
CTHER INFORMATION: Cyclic Peptide may comprise N-terminal
CTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
CTHER INFORMATION: and/or C-terminal modifications such as amide or
CTHER INFORMATION: ester group
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100.0%; Score 34; DB 4; I
100.0%; Pred. No. 4.1e+05;
                                                               0; Mismatches
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Gaps

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Sequence 96, Application US/09458870;
Sequence 96, Application US/09458870;
Patent No. 6458427;
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Farockhi, Riaz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILLE REFERENCE: 100086-401C8;
CURRENT APPLICANTON NUMBER: US/09/458,870
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 96
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                  RESULT 33
US-09-458-870-90
; Sequence 90, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farockhi, Rlaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; TITLE OF INVENTION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SEQ ID NO 90
; SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; PEATURE: OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-458-870-90
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group ; OTHER INFORMATION: and/or C-terminal modifications such as amide or ; OTHER INFORMATION: ester group US-09-458-870-89
                                                                                                                             Length 7;
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-544-782-93
i Sequence 93, Application US/09544782
i Sequence 93, Application US/09544782
i Patent No. 6610821
i GENERAL INFORMATION:
i APPLICANT: Blaschuk, Orest W.
i APPLICANT: Gour, Barbara J.
i APPLICANT: Farookhi, Riaz
i APPLICANT: Ali, Annar
i TILE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
i FILE REFERENCE: 100086.401C9
i CURRENT APPLICATION NUMBER: US/09/544,782
i CURRENT FILING DATE: 2000-04-07
i NUMBER OF SEQ ID NOS: 96
i SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
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APPLICANT: Barbara J.
APPLICANT: Farookhi, Riaz
APPLICANT: Farookhi, Riaz
APPLICANT: Annar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401C8
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
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                                                                              100.0%; Score 34; DB 4; L
100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0;
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; Sequence 89, Application US/09458870
; Pertent No. 6465427
; GENERAL INFORMATION:
       ; OTHER INFORMATION: ester group US-09-544-782-92
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ORGANISM: Artificial Sequence
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LENGTH: 6
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TYPE: PRT
ORGANISM: Artificial Sequence
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FEATURE:
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; Sequence 89, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Parockhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT FALING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
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Sequence 90, Application US/09544782
Patent No. 6610821
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Barbara J.
APPLICANT: Parookhi, Riaz
APPLICANT: Parookhi, Riaz
APPLICANT: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION FILE REFERENCE: 100086.401C9
CURRENT APPLICATION NUMBER: US/09/544,782
CURRENT PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-544-782-89
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                                    CTHER INFORMATION: Cyclic Peptide may comprise N-terminal
CTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
CTHER INFORMATION: and/or C-terminal modifications such as amide or
CTHER INFORMATION: ester group
US-09-458-870-96
  OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
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100.0%; Pred. No. 4.1e+05;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-544-782-89
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LENGTH: 7
                                                                                                                                                                 Query Match
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Sequence 95, Application US/09458870

Patent No. 6465427

GENERAL INFORMATION:
APPLICANT: Barbara J.
APPLICANT: Farockhi, Riaz
APPLICANT: Ali Anmar

TILLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TILLE REFERENCE: 100086.401C8
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT PILLING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 95
LINGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Farookhi, Riaz
APPLICANT: Ali, Anmar
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION FILE REFERENCE: 100086.401C9
CURRENT APPLICATION NUMBER: US/09/544,782
CURRENT APPLICATION NUMBER: US/09/544,782
SURBER OF SOFTWARE: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or; OTHER INFORMATION: ester group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                    Gaps
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence OTHER INFORMATION: Cyclic Peptide may comprise N.terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-544-782-90
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100.0%; Pred. No. 4.1e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    0; Mismatches
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Patent No. 6610821
GENERAL INFORMATION:
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Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
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Best Local Similarity
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Patent No. 6610821
CABREAL INFORMATION:
APPLICANT: Barbara J.
APPLICANT: Farookhi, Riaz
APPLICANT: Rarookhi, Riaz
APPLICANT: Toolhi, Anmar
APPLICANT: APPLICANT: POOR MODULATING CELL ADHESION FILE REFERENCE: 100086.401C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Alary Annar.
APPLICANT: Alary Annar.
APPLICANT: Ali Annar.
APPLICANT: Ali Annar.
APPLICANT: Ali Annar.
APPLICANT: Ali Annar.
COMPRENT: Ali Annar.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION TITLE OF INVENTENT: 100086.401C8
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 101
LENGTH: 8
LENGTH: 8
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                                      OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
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                                                                                FEATURE:
CTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
US-09-458-870-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
FEATURE:
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; OTHER INFORMATION: Where Xaa is beta, beta-dimethyl cysteine
US-09-458-870-101
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100.0%; Pred. No. 4.1e+05;
/ative 0; Mismatches 0;
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Patent No. 6465427
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Best Local Similarity
5; Conserve
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LOCATION: (5)
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GENERAL INPORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
CURRENT APPLICATION NUMBER: US/09/544,782

CURRENT FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 96

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 95

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: madification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: ester group
US-09-544-782-95
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 4; I
100.0%; Pred. No. 4.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 213, Application US/08311731A Patent No. 6583266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 617/720-2441
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
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Gape
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; Sequence 30, Application US/09347878C
; Sequence 30, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 22885-1651
; CURRENT PILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
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APPLICANT: Baneriee, Debabrata
APPLICANT: Tong, Youzhi
APPLICANT: Liu-Chen, Xinyue
TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof
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                                                 APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Hardwick, J. Marie
APPLICANT: Reitz, Marvin
FILLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
TITLE OF INVENTION: Associated Herpesvirus
FILLE REFERENCE: 1107.78372
CURRENT FILLIG DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/022,591
PRIOR APPLICATION NUMBER: 1999-07-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Human thymidylate synthase protein sequence public publication infoRMATION:
DATABASE ACCESSION NUMBER: D00596/GenBank
US-09-347-878-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 312;
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80.0%; Pred. No. 4e+02;
iive 1; Mismatches
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Pred. No. 4e+02;
1; Mismatches
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Best Local Similarity 80.0.
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Best Local Similarity 80.0.
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PAPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
RIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7794
                                                                                                                                                                                                                   FACENTAL NO. 981233

FACENTERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLO01307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEG FOR WINDOWS VERSION 4.0

SEQ ID NO 10680
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  0; Indels
  0; Mismatches
                                                                                                                                                                            Sequence 10680, Application US/09949016 Patent No. 6812339
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Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 34, Application US/09230637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Eachan 4; Conservative
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  5; Conservative
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Best Local Similarity
Matches 4; Conserv
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65 CHAIC 69
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                                        1 CHAVC 5
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                                                                                 1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                  US-09-949-016-10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-016-10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 43
US-09-543-681A-7794
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US-09-230-637-34
  Matches
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Sequence 7293, Application US/09328352
Fadent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.2%; Score 31; DB 4; Length 760;
80.0%; Pred. No. 8.7e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HER4 HUMAN RECEPTOR TYROSINE KINASE
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,708A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08484438
Patent No. 5811098
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D. APPLICANT: Shoyab, Mohammed
APPLICANT: Shoyab, Mohammed
APPLICANT: Hellstr m, Karl E.
APPLICANT: Hellstr m, Rarl E.
APPLICANT: Hellstr m, Rarl E.
TITLE OF INVENTION: HER4 HUMAN RECEPE
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7293
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olecki, Nancy
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                      91320-1789
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                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-328-352-7293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-336-708A-9
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US-08-484-438-7
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; Sequence 10160, Application US/09949016
; Patcent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION WUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/214,755
; PRIOR APPLICATION NUMBER: 60/214,755
; PRIOR PILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE:
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                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Wild type human thymidylate synthase amino acid CTHER INFORMATION: sequence (Genbank Accession number NP001062) US-09-367-007C-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.2%; Score 31; DB 4; Length 313;
80.0%; Pred. No. 4e+02;
tive 1; Mismatches 0; Indels
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APPLICANT: Pacifici, Robert E.
APPLICANT: Thomason, Arlen R.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Hybrid Receptor Molecules
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
FILE REFERENCE: D5978
CURRENT APPLICATION WUMBER: US/09/367,007C
CURRENT FILING DATE: 1999-10-15
FRIOR APPLICATION NUMBER: PCT/US98/02145
PRIOR FILING DATE: 1998-01-03
NUMBER OF SEQ ID NOS: 39
LENGTH: 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
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US-09-949-016-10160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Human
US-09-949-016-10160
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Pred. No. 1.3e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1210;
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| Patent No. 6031072
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. APPLICANT: Gour, Barbara J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING TITLE OF INVENTION: CELL ADHESION NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selectable cell surface marker genes
          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,035

FILING DATE: 7 Jun 1995

CLASSIFCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PERTYMAN, David G.

REGISTRATION NUMBER: 33 438

REGISTRATION NUMBER: 33 438

RETERENCE/DOCKET NUMBER: 1414.656

TELEPHONE: 404/688-9880

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1210 amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                  91.2%; Score 31; DB 2;
80.0%; Pred. No. 1.3e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WOVARTIS AG
APPLICANT: VERES, GABOR
APPLICANT: PIPPIG, SUSANNE
APPLICANT: PIPPIG, SUSANNE
TITLE OF INVENTION: Gelectable cell surfact
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/715,249
CURRENT PILING DATE: 1000-11-17
PRIOR APPLICATION NUMBER: us 60/166594
PRIOR PILING DATE: 1999-11-19
PRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2
LENGTH: 1210
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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506 CHALC 510
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; ORGANISM: EGFR
US-09-715-249-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-893-534A-9
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Sequence 4, Application US/08475035;
Batent No. 598553;
GENERAL INFORMATION:
APPLICANT: KRING, C. R.
APPLICANT: ARRONSON, STUART A.
TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM TITLE OF INVENTION: EGF RECEPTOR GENE
NUMBER OF SEQUENCES:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/120,704
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: US 07/981,165
FILING DATE: 10-NOV-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION NUMBER: 18,872
RETERENCE/DOCKET NUMBER: 524-230
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
CUNDE: Amino acids
TWORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                       ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.2
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                               STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: unki
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:|
506 CHALC 510
                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CHAVC 5
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US-08-475-035-4
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gequence 20, Application US/09115395A

| Sequence 20, Application US/09115395A
| Patent No. 6207639
| Gentral No. 6207639
| Gentral No. 6207639
| Gentral No. 6207639
| Gentral Statement On Compounds and Methods For Modulating Neurite Courcert No. Compounds and Methods For Modulating Neurite Courcert Pillor Courcert No. Compounds and Methods For Modulating Neurite Courcert Application Number: US/09/115,395A
| CURRENT FILING DATE: 1998-07-14
| CARLIER APPLICATION NUMBER: US/99/679
| EARLIER PILLING DATE: 1997-07-11
| EARLIER PILLING DATE: 1997-07-11
| EARLIER PILLING DATE: 1996-07-12
| NUMBER OF SEQ ID NOS: 77
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NOS: 77
                                                                                                                                                                                                                                                              Gaps
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-115-195-20
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US-09-507-102-9
; Sequence 9, Application US/09507102
; Patent No. 6325452
; Patent No. 6326352
; APPLICANT: Blaschuk, Orest W.
Gour, Barbara J.
; TILLE OF INVENTION: CELL ADHESION
CELL ADHESION
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ADDRESSEE: SEED IP LAW GROUP PLLC
STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
                                                                                                                                                                                                                 88.2%; Score 30; DB 3; Length 5; 80.0%; Pred. No. 4.1e+05; ive 0; Mismatches 1; Indels
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STATE: Washington
COUNTRY: USA
ZIP: 98104
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: S amino acids
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Best Local Similarity 80.v-
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                         ; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-996-679-9
                                                                                     amino acid
                                                                                                                                                                                                                                                                                                       1 CHAVC 5
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                                                                                                       STRANDEDNESS:
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US-09-115-395-20
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US-08-996-679-9
is Sequence 9, Application US/08996679
is Sequence 9, Application US/08996679
is Patent No. 6168071
is GENERAL INFORMATION:
is APPLICANT: Barbara J.
itTLE OF INVENTION: CELL ADHESION
itTLE OF INVENTION: CELL ADHESION
invERS OF SEQUENCES: 63
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: SEED and BERRY LLP
is STREET: 6300 Columbia Center, 701 Fifth Avenue
is STREET: Machington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5;
                                                                                                              COUNTRY: USD.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIND DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,534A
FILING DATE: 11-JUL-1997
CLASSIFICATION: 530
ATTORNEY/ACRIT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 100086.401
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (206) 622-4900
TELEFRAX: (206) 622-4900
TELEFRAX: C106) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNE: Washington
CUMTRY: USA
ZIP: 98104
COMPUTER READBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,679
FILING DATE: 23-DEC-1997
CLASSIFICATION:
                    ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%; Score 30; DB 3; I
80.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 1;
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NAME: Maki, Daivd J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 100086.401C1
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular;
MOLECULE TYPE: peptide
US-08-893-534A-9
  CORRESPONDENCE ADDRESS:
                                                                                       Washington
: USA
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                                                                 CITY: Sea
STATE: Wa
COUNTRY:
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Glaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TITLE OF INVENTION: USOPOUNDS AND METHODS FOR MODULATING CELL ADHESION
TITLE OF INVENTION: 100065-401C5
CURRENT APPLICATION NUMBER: 105/02/10
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 5
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FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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; Sequence 11, Application US/09357717
; Patent No. 6417325
; GENERAL INFORMATION:
                                                                                            US-09-248-074-11
; Sequence 11, Application US/09248074
; Patent No. 6346512
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Best Local Similarity
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US-09-250-059-11

Sequence 11, Application US/09250059

Patent No. 6333307

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
FILLE REPRENCE: 100066-401C6

CURRENT APPLICATION NUMBER: US/09/250,059

CURRENT PILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 87

SEQ ID NO 11

LENGTH: 5
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                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SUSTEM: SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/507,102

FILING DATE: 17-Feb-200

CLASSIFICATION: «Inhrown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/893,534

FILING DATE: 11-JUL-1997

APPLICATION NUMBER: US 60/021,612

FILING DATE: 12-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 100086.401C10

TELECOMMUNICATION: INFORMATION:

TELECOMMUNICATION: INFORMATION:

TELECOMMUNICATION: INFORMATION:
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80.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 1;
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-507-102-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
  COMPUTER READABLE FORM:
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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CRGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: Cyclic
OTHER INFORMATION: Control peptide
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
CHER INFORMATION: ester group
US-09-544-782-11
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic OTHER INFORMATION: control peptide and COTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Farockhi, Riaz
TILE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
FILE REPRENCE: 100086, 401C12
CURRENT FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%; Score 30; DB 4; Length 5; 80.0%; Pred. No. 4.1e+05; tive 0; Mismatches 1; Indels
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                                                                                                                                  Sequence 11, Application US/09544782 Patent No. 6610821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10058821
Patent No. 6780845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                      APPLICANT: Blaschuk, Orest W. APPLICANT: Gour, Barbara J. APPLICANT: Farookhi, Riaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.07
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CHAVC 5
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CHGVC :
                                                                                                            US-09-544-782-11
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US-10-058-821-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                            APPLICANT: Baschuk, Orest W.
APPLICANT: Baschuk, Orest W.
APPLICANT: Barbara J.
APPLICANT: Farookhi, Riaz
APPLICANT: Farookhi, Riaz
APPLICANT: Ali, Anmax
TITLE OF INVANTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.40108
CURRENT APPLICATION NUMBER: US/09/458,870
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 101
SEQ ID NOS: 101
LENGTH: 5
LENGTH: 5
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/09248015

Sequence 20, Application US/09248015

Setent No. 6562786

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Blaschuk, Orest W.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS

FILE REFERENCE: 100086.401C4

CURRENT APPLICATION NUMBER: US/09/248,015

NUMBER OF SEQ ID NOS: 81

SOFTWARE PATENTING DATE: 1999-02-10

SEQ ID NO 20

LENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Cyclic OTHER INFORMATION: control peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Cyclic OTHER INFORMATION: control peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.2%; Score 30; DB 4; Length 5; 80.0%; Pred. No. 4.1e+05; 1:ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 4; Length 5; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
                                                                                                            Sequence 11, Application US/09458870; Patent No. 6465427; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.2%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 4, Conservative
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Best Local Similarity
       CHGVC 5
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                                                                    RESULT 60
US-09-458-870-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/08331625A
Patent No. 6057436
GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
APPLICANT: Reed, Albert Paul
APPLICANT: Nones, Elaine V.
TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/331,625A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPTCATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/880,194
FILING DATE: 08-MAY-1992
PRIOR APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-MOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
RESERRACE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                    FILE REFERENCE: 2314-242
CURRENT APPLICATION NUMBER: US/09/910,009A
CURRENT FILING DATE: 2001-07-23
FRIOR APPLICATION NUMBER: US 60/219,619
FRIOR FILING DATE: 2000-07-21
FRIOR FILING DATE: 2000-11-03
FRIOR FILING DATE: 2000-11-03
FRIOR FILING DATE: 2001-129
FRIOR FILING DATE: 2001-01-29
FRIOR APPLICATION NUMBER: US 60/245,157
FRIOR FILING DATE: 2001-01-29
FRIOR APPLICATION NUMBER: US 60/277,270
FRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SEQ ID NO 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: Mu-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CONGANISM: Conus aulicus
US-09-910-009A-454
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7, CHSIC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(16)
; OTHER INFORMATION: Xaa at residue 5 and 6 is Pro or Hyp
US-09-910-009A-358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivers, Baldomero M.
APPLICANT: MINCHOS, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
                                                                                                                                                                                              Journal of Utah Research Foundation Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Garrett, James B.
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shen, Greg S.
APPLICANT: Magataff, John D.
TILE REPERENCE: 2314-242
CURRENT FILIDE DATE: 2001-07-23
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PARENTH FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-910-009A-454; Sequence 454, Application US/09910009A; Patent No. 6727226; GENERAL INFORMATION:
                                                                                                                 US-09-910-009A-358
; Sequence 358, Application US/09910009A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones, Robert M.
Cartier, G. Edward
Shen, Greg S.
Wagstaff, John D.
                                                                                                                                                                                                                                                                                                                                                                                                        Jones, Robert M.
Cartier, G. Edward
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Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                       Cruz, Lourdes J.
Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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ORGANISM: Conus aulicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||::|
7 CHSIC 11
    1 CHGVC 5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
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                                                                                                               COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRUT APPLICATION DATE:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 4;
Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-03n-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: 40nknown-
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 69
8-05-910-009A-357
; Sequence 357, Application US/09910009A
; Patent No. 6727226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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Best Local Similarity
3, Conserve
                                                        8 CHSIC 12
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8 CHSIC 12
                      CHAVC 5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/09494151
Sequence 35, Application US/09494151
Patent No. 6372224
GENERAL INFORMATION:
AMiller, Timothy J.
Klepfer, Sharon
Reed, Albert Paul
Gones, Elaine V.
TITLE OF INVENTION: Canine Coronavirue S Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
CLASSIFICATION: vUnknown>
PRIOR APPLICATION ON AUNKNOWN>
PRIOR APPLICATION NUMBER: 08/331,625
                                                                                                                                                                    DB 3; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 3; Length 17;
Pred. No. 46;
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SCHECK, PATTICIA A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-494-151-35
                                                                                                                                                                    88.2%; Score 30;
60.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patents
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Best Local Similarity 60.0%;

Matches 3; Conservative
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acid
                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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CHSIC 12
                                                                                                                                                                                                                                            1 CHAVC 5
                                                                                                                                US-08-331-625A-35
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US-09-494-151-35
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GENERAL INCORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: uS/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 55116
LENGTH: 165
GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 39999
LENGTH: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 88.2%; Score 30; DB 4; Length 165
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSER: SmithKline Beecham Corporation - Corporate
ADDRESSER: Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Indels
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Patent No. 6057436
GENERAL INFORMATION:
APPLICANT: Klepfer, Sharon
APPLICANT: Reed, Albert Paul
APPLICANT: Jones, Elaine V.
TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 4; I pred. No. 3.3e+02; 0; Mismatches I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-55116
                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 55116, Application US/09270767; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 80.0.
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CORRESPONDENCE ADDRESS:
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US-09-270-767-55116
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 4; Length 65;
Pred. No. 1.5e+02;
2; Mismatches 0; Indels
                     University of Utah Research Foundation Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Garrett, James E.
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shen, Greg S.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: Mn. Conopeptides
TITLE REPERENCE: 2314-242
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219, 619
PRIOR APPLICATION NUMBER: US 60/219, 619
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2001-10-39
PRIOR FILING DATE: 2001-01-39
PRIOR FILING DATE: 2001-01
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-3
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PARENT PA
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Patent No. 6562958
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                                                                                                                                                                                                                                                                                 Jones, Robert M.
Cartier, G. Edward
                                                                                                                                                                                                Cruz, Lourdes J.
Shon, Ki-Joon
Jacobsen, Richard
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Best Local Similarity 60.v
and 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Conus aulicus
US-09-910-009A-357
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55 CHSIC 59
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13 CHSIC 17
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US-09-270-767-39899
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APPLICANT:
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ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: AUNKNOWN>
PRIOR APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
APPLICATION NUMBER: US/09/494,151
FILING DATE: 4UNKNOWN>
APPLICATION NUMBER: US/09/494,151
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
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Reed, Albert Paul
Jones, Blaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.2%; Score 30; DB 3; Length 203; 60.0%; Pred. No. 4e+02; ive 2; Mismatches 0; Indels
                                                       FILING DATE: CURROWN APPLICATION WUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-MOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: SBC H85010-1
FELECOMMUNICATION INFORMATION:
TELEPRAY: (215) 270-5015
TELEPRAY: (215) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | LENGTH: 203 amino acids | TYPE: amino acids | TYPE: amino acid | TOPOLOGY: unknown | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-09-494-151-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,625
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Patent No. 6602504
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miller, Timothy J.
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Best Local Similarity
Matches 3; Conserva
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182 CHSIC 186
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US-09-972-484-11
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 3; Length 203;
Pred. No. 4e+02;
2; Mismatches 0; Indels
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Klepfer, Sharon
Reed, Albert Paul
Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
                                                                                                                                                                                                                                                                                                           CLASS PRIOR 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/880,194
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/494,151
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                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09494151; Patent No. 6372224; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: PA
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60.0%;
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amino acid
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Best Local Similarity 60.0
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-331-625A-11
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CHSIC 186
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| APPLICANT: Worley, Paul F. |
| APPLICANT: Worley, Paul F. |
| APPLICANT: Gorder, Bernard |
| APPLICANT: Gorder, Bernard |
| APPLICANT: Heimisch, Holger |
| APPLICANT: Scheek, Sigrid |
| APPLICANT: MANDICAN |
| TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE |
| TITLE OF INVENTION: IMMEDIATE |
| TITLE OF INVENTION OF 1999-02-05 |
| CURRENT FILING DATE: 1999-02-06 |
| PRIOR APPLICATION NUMBER: 60/074,135 |
| PRIOR APPLICATION NUMBER: 60/074,135 |
| PRIOR APPLICATION NUMBER: 60/074,135 |
| PRIOR PLING DATE: 1998-02-06 |
| NUMBER OF SEQ ID NOS: 62 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 62 |
| TENGTH: 342 |
| TENGTH: DATE: 1998-02-06 |
| WADEL DATE: 1998-02-06 |
| SEQ ID NO 62 |
| SEQ ID NO 62 |
| TENGTH: 342 |
| TENGTH: DATE: 1998-02-06 |
| TENGTH: 1908-02-06 |
| TENGTH: 1908-02-06 |
| SEQ ID NO 62 |
| TENGTH: 1908-02-06 |
| TENGTH: 190
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Sequence 85. Application US/07857224B

GENERAL INFORMATION:

APPLICANT: Benner, Steven A.

TILE OF INVENTION:

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSE: Steven A. Benner

STREET: Hadlaubstrasse 151

CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: Switzerland
ZIP: (note: this is an international post code) CH-8092
ZIP: (note: this is an international post code) CH-8092
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,2248
FILING DATE: 0./25/92
Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 342,
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Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
                                                                 1; Indels
n 88.2%; Score 30; DB 4; I Similarity 80.0%; Pred. No. 5.6e+02; 4; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                               Sequence 62, Application US/09244805
Patent No. 6699660
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PRIOR APPLICATION DATA: none
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CORGANISM: Homo sapiens
US-09-244-805-62
                             Best Local Similarity
Matches 4; Conserv
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US-07-857-224B-85
                                                                                                                                                                                                                                                                                                                        US-09-244-805-62
         Query Match
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Batent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERSENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Facton, NO. 002344, |
| GENERAL INFORMATION: |
| APPLICANT: Goldman, Barry S. |
| APPLICANT: Goldman, Barry S. |
| APPLICANT: Galdman, Steven C. |
| APPLICANT: States, Steven C. |
| APPLICANT: Wiegand, Roger C. |
| TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10(15849)B |
| FILE REPRENCE: 38-10(15849)B |
| CURRENT RELING DATE: 2001-07-10 |
| PRIOR APPLICATION NUMBER: 60/217,883 |
| PRIOR FILING DATE: 2000-07-10 |
| NUMBER OF SEQ ID NOS: 16825 |
| SEQ ID NO 15175 |
| LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 30; DB 4; Length 203; 60.0%; Pred. No. 4e+02; 1. dismatches 0; Indels
             REFERENCE/DOCKET NUMBER: SBC H85010-1
                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-902-540-15175
; Sequence 15175, Application US/09902540
; Patent No. 6833447
                                       TELECOMMUNICATION INFORMATION:
TELEPRONE: (215) 270-5015
TELEPRONE: (215) 270-5016
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH 2 203 amino acids
TYPE: amino acids
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Myxococcus xanthus
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Best Local Similarity
Matches 4; Conserv
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182 CHSIC 186
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US-09-489-039A-9117
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Gaps

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; Sequence 52, Application US/08331625A; Patent No. 657436; Batent No. 657436; Batent No. 657436; Batent No. APPLICANT: Miller, Timothy J. APPLICANT: Reed, Albert Paul APPLICANT: Reed, Albert Paul APPLICANT: Jones, Elaine V. TITLE OF INVENTION: Therefor NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: 59 CORRESPONDENCE ADDRESS: ADDRESSE: Patents.
                                                                                                                                                                                           88.2%; Score 30; DB 4; Length 777; 80.0%; Pred. No. 1.3e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIE: 19406-27'9

ZIE: 19406-27'9

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/331,625A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-44409
FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767 CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 44409 LENGTH: 777
                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                     FEATURE:
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; Sequence 44409, Application US/09270767
; Parent No. 6703491.
; GRNERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
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                                                                                                                                                                                                                                AUTHORS: Joernvall, H.
AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TILE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
PAGES: 4226-4230
DATE: 1981
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Pred. No. 9.1e+02;
0; Mismatches 1; Indels
                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: mouse
FATURE: Alcohol dehydrogenase, Table 3 Column 6
PUBLICATION: INFORMATION:
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.2%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                               TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 CHAAC 286
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-2799
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: DSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-OCt-2001
CLASSIFICATION: CURNOWN>
                                                                                                                                                                  TITLE OF INVENTION: Canine Coronavirus S Gene and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08308872B
Sequence 2, Application US/08308872B
Patent No. 5661006
GENERAL INFORMATION
APPLICANT: BROWN, Thomas David Kay
APPLICANT: HORSBURGH, Brian Colin
TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5661006el Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.2%; Score 30; DB 4; Le. 60.0%; Pred. No. 1.7e+03; ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: cUnknown>
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
FILING DATE: 13-MAY-1991
FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-972-484-52
                                                                                                                                                                                                                                                                                                STREET: 709 Swedeland Road
             Sequence 52, Application US/09972484
Patent No. 6602504
GENERAL INFORMATION:
APPLICANT: Kiepfer, Sharon
Reed, Albert Paul
                                                                                                                                                ones, Elaine V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              Patents
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity 60.0
Matches 3; Conservative
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US-08-308-872B-2
US-09-972-484-52
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ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
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Pred. No. 1.7e+03;
2; Mismatches 0; Indels
                                          Length 1101;
                                                                                                                                                                                                                                                                              Sequence 52, Application US/09494151
Patent No. 6372224
GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
Klepfer, Sharon
Reed, Albert Paul
Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 1946-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAWBER: US/09/494,151
FILING DATE: 28-Jan-2000
CLASSIFICATION: <UNKNOWN>
                                                                                   0; Indels
                                      88.2%; Score 30; DB 3; 50.0%; Pred. No. 1.7e+03; ive 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,625
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 07/699,927
FILING DATE: 13-MAX-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 114-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOLKCULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-494-151-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 709 Swedeland Road CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                        Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: PA
COUNTRY: USA
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                                                                                                                                                       1080 CHSIC 1084
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                                                                                                                              1 CHAVC 5
  US-08-331-625A-52
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RESULT 84

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Length 1101;

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0; Gaps
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Sequence 2, Application US/08331625A

Batent No. 6057436

GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
APPLICANT: Reed, Albert Paul
APPLICANT: Reed, Albert Paul
APPLICANT: Jones, Elaine V.
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: MatthKline Beecham Corporation - Corporate
ADDRESSEE: Patents
ADDRESSEE: Patents
ADDRESSEE: Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 1; Length 1451;
Pred. No. 2.2e+03;
2; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,872B
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,846
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 07/872,641
FILING DATE: 26-APR-1992
PRIOR APPLICATION NUMBER: BP 91.303.737.0
FILING DATE: 25-APR-1991
FILING DATE: 25-APR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GORANLEY, MAY E.
REGISTRATION NUMBER: 34 409
TELECOMMUNICATION INFORMATION:
NEGISTRATION NUMBER: 34 409
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 358-5200
INFORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1451 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..1451
OTHER INFORMATION: /label= CCVInSAVC-1_Spike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine corona virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 709 Swedeland Road CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Canine co
STRAIN: CCVINSAVC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1430 CHSIC 1434
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; Sequence 4, Application US/08308872B
; Patent No. 5661006
; GENERAL INFORMATION:
   APPLICANT: BROWN, Thomas David Kay
   APPLICANT: HORSBURGH, Brian Colin
   TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE
   NUMBER OF SEQUENCES: 9
   CORRESPONDENCE ADDRESS:
   ADDRESSE: Akzo No. 5661006el Patent Department
   STREET: Nazyland
   STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%; Score 30; DB 1; Length 1443; 60.0%; Pred. No. 2.2e+03; tive 2; Mismatches 0; Indels
                                                                                                                 COMPUTER READABLE FORM:
MEDLUM TYPE: Ploppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,872B
FILING DATE: 19-SEP-1994
PRIOR APPLICATION NUMBER: US 08/042,846
FILING DATE: 05-APR-1993
PRIOR APPLICATION NUMBER: US 08/042,846
FILING DATE: 24-APR-1993
PRIOR APPLICATION NUMBER: US 07/872,641
FILING DATE: 25-APR-1992
PRIOR APPLICATION NUMBER: B 1.303.737.0
FILING DATE: 25-APR-1991
CLASSIFICATION WINDER: 34,409
TELECOMMUNICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 334,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: AMIN OR SEL
      STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville STATE: Maryland COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
LOCATION: 1..1443
INFORMATION: /label= CCV6_Spike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
ORGINAL SOURCE:
ORGANISM: Canina corona virus
STRAIN: CCV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60..
Best Local 3; Conservative
                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||::|
1422 CHSIC 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CHAVC 5
                                                                          COUNTRY: UZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 86
US-08-308-872B-4
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ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patents
                                                                                                                                                                                                                                                                                                                                                                    Length 1452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09972484
Sequence 2, Application US/09972484
Patent No. 6602504
GENERAL INFORMATION:
Klepfer, Timothy J.
Klepfer, Sharon
Reed, Albert Paul
Jones, Elaine V.
TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 3;
Pred. No. 2.2e+03;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-0an-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Schreck, Patricia A.
                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                          88.2%;
60.0%;
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 59
                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1431 CHSIC 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CHAVC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-972-484-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
Patente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 1452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 3; I
Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Paceful in Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-2an-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: 08/331,625
FILING DATE: 13-MAX-1991
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAX-1991
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAX-1991
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAX-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: SCHECK, PMELICATION
NUMBER: SCHECK PMELICATION
NUMBER: SCHECK
                   PRIOR AFFLICATION NUMBER: US 07/880,194
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 270-5015
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Miller, Timothy J.
Klepfer, Sharon
Reed, Albert Paul
Jones, Elaine V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09494151
Patent No. 6372224
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-331-625A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1431 CHSIC 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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1 CHAVC 5
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US-08-392-459-22
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                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                   Gaps
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                                                                                                                                                                                                                          RESULT 90
PCT-US93-04384-18
; Sequence 18 Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Miller, Timothy J.
; APPLICANT: Alege fer, Sharon
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patente
; STREET: 709 Swedeland Road
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                   88.2%; Score 30; DB 4; Length 1452; 60.0%; Pred. No. 2.2e+03; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTE: FA

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURERY APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04384
FILING DATE: 19930S07
CLASSIFICATION NUMBER: PCT/US93/04384
FILING DATE: 08-MAY-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: 33,777
REFERENCE CAPACET INFORMATION:
NUMBE: SCHIECK, PATLICA A.
REGISTRATION NUMBER: 33,777
REFERENCE CAPACET INFORMATION:
TELEPHONE: (215) 270-5095
INFORMATION FOR SEO ID NO: 18:
SEQUENT: LASZ amino acide

LENGTH: LASZ amino acide

"WDD: LENGTH: LASZ amino acide
"WDD: LENGTH: LASZ amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F: 709 Swedeland Road
King of Prussia
                                       Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 3, Conservative
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US-09-972-484-2
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RESULT 91

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SEGURATION TO PROMATION TO PCTUG9304692

APPLICANT: Algaber, Sharon
APPLICANT: Algaber, APPLICANT: Algaber, APPLICANT: Algaber, APPLICANT: Algaber, APPLICANT: Algaber, APPLICANT: APPLICANT: Algaber, APPLICANT: APPLICANT:
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 amino acids
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 60.0.
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                                                                                                                                                                                                           ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-392-459-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                1 CHAVC 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26. Application US/08392459
; Patent No. 6280974
; GENERAL INFORMATION:
    APPLICANT: SmithKline Beecham, Corporation
    TITLE OF INVENTION: Proteins
    TITLE OF INVENTION: Proteins
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: SmithKline Beecham Corporation
    STREET: 709 Swedeland Road
    CITY: King of Prubsia
                  COUNTRY: USA

ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,459
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,459
                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
NAME: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: 5BC 14532B
TELECOMMINICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-WAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZOP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMBALIble
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5015
TELEFAXION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 1454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0.
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MOLECULE TYPE: protein
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1433 CHSIC 1437
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US-08-392-459-26
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Pred. No. 2.2e+03;
2; Mismatches 0; Indels
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Patent No. 6642359
GENERAL INPORMATION:
APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: King, William T.
REGISTRATION NUMBER: 30,954
REGISTRATION NUMBER: SBC 14532B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
TELECHONE: 721570-5015
TELEPAN: (215) 270-5016
TELEPAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 1454 emino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-854-799-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30;
Pred. No.
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88.2%; Score 30; DB 5; Length 1454; 60.0%; Pred. No. 2.2e+03; ive 2; Mismatches 0; Indels
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FRESUL: 197

GENERAL INFORMATION: Statishing the Coronavirus STITLE OF INVENTION: Recombinant Feline Coronavirus STITLE OF INVENTION: Recombinant Feline Coronavirus STITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road

CITY: King of Prussia STATE: PA

COUNTY: USA

STATE: PA

COMPUTER: ISA

COMPUTER: ISA

COMPUTER: ISA

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/08525

FILING DATE: 19911114

CLASSIFICATION NUMBER: US 07/698,927

FILING DATE: 13-MAY-1991

PRIOR APPLICATION UNDER: US 07/613,066

FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:
STATE: PA

COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMET PC-DOS/MS-DOS
SOFTWARE: PATEMET Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08525
FLING DATE: 19911114
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEMEPHONE: (215) 270-5015
TELEFAX: (215) 270-5015
TELEFAX: (215) 270-5090
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 amino
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein
PCT-US91-08525-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1433 CHSIC 1437
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COUNTRY: USA

CONDUTER READABLE FORM:
MEDDIUM TYPE: Ploppy disk
MEDRIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATA:
MEDLICATION DATA:
APPLICATION NUMBER: US/09/854,799
FILING DATE: 14-May-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,459
FILING DATE: cUnknown>
APPLICATION NUMBER: 08/392,459
FILING DATE: cUnknown>
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1454;
                                                                                                                                  RESULT 95
US-09-854-799-26
; Sequence 26, Application US/09854799
; Patent No. 6642359
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Proteins
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PCT-US91-08525-22
; Sequence 2.2. Application PC/TUS9108525
; GENERAL INFORMATION:
; TITLE OF INVENTION: Recombinant Feline Coronavirus S; TITLE OF INVENTION: Proteins
; VUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%; Score 30; DB 4; Length 145
60.0%; Pred. No. 2.2e+03;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-854-799-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (215) 270-1
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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                                                              1433 CHSIC 1437
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Gaps

Gaps

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PCT-US93-04384-8

Sequence 8, Application PC/TUS9304384

Sequence 8, Application PC/TUS9304384

GENERAL INFORMATION:

APPLICANT: Miller, Timothy J.

APPLICANT: Reed, Albert Paul

APPLICANT: Reed, Albert Paul

APPLICANT: Jones, Blaine V.

TITLE OF INVENTION: Compositions and Methods for Vaccination

TITLE OF INVENTION: Against Coronaviruses

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patents

ADDRESSEE: Patents

ADDRESSEE: Patents

ADDRESSEE: Patents
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                                       Score 30; DB 5; Length 1454;
Pred. No. 2.2e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04384
FLING DATE: 19930507
FLING DATE: 19930507
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,171
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATPONEY/AGENT INPOMMATION:
NAME: SCHECK, PATAICA A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
RELEBENOME: (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 709 Swedeland Road CITY: King of Pruseia
                                               88.2%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (215) 270-5090 INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS:
                                                 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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1433 CHSIC 1437
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    PCT-US93-04384-2
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APPLICANT: Klepfer, Sharon
APPLICANT: Reed, Albert Paul
APPLICANT: Reed, Albert Paul
APPLICANT: Conces, Blaine V.
TITLE OF INVENTION: Compositions and Methods for Vaccination
TITLE OF INVENTION: Against Coronaviruses
NUMBER OF SECURENCE: 48
ADDRESSEE: SmithKline Beecham Corporation - Corporate
ADDRESSEE: SmithKline Becham Corporation - Corporate
                                                                                                                                                                                                                                                                                                                                        88.2%; Score 30; DB 5; Length 1454;
60.0%; Pred. No. 2.2e+03;
tive 2; Mismatches 0; Indels
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ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US93/04384
FILING DATE: 1930507
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,171
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: SCHIECK, PETRICA A.
REGISTRATION NUMBER: 33,77
REFERENCE/DOCKET NUMBER: SEC H85009-1
TELECOMMUNICATION INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SEC 14532B
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-04384-2
; Sequence 2, Application PC/TUS9304384
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                               LENGTH: 1454 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-08525-26
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1433 CHSIC 1437
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Sequence 16, Application PC/TUS9304384

Sequence 16, Application PC/TUS9304384

GENERAL INFORMATION;
APPLICANT: Miller, Timothy J.
APPLICANT: Reed, Albert Paul
APPLICANT: Reed, Albert Paul
APPLICANT: Reed, Albert Paul
APPLICANT: Compositions and Methods for Vaccination
ITTLE OF INVENTION: Compositions and Methods for Vaccination
ITTLE OF INVENTION: Against Coronaviruses
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patents
ADDRESSEE: Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19406-2799
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SOFTWARE: PETLOATION DATA:
APPLICATION NUMBER: PCT/US93/04384
FILING DATE: 1930807
FILING DATE: 13-MAY-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
FRIOR APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY AGENT INFORMATION:
NAME: Schreck, Patrica A.
REGISTRATION NUMBER: SBC H85009-1
TELEPHONE: (215) 270-5015
TELEPHONE: (215) 270-5015
TELEPHONE: (215) 270-5030
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1444 amino acids
TYPE: AMINO ACID
TOPOLOGY: Inear
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ö 88.2%; Score 30; DB 5; Length 1454; 60.0%; Pred. No. 2.2e+03; Live 2; Mismatches 0; Indels Best Local Similarity 60.0 Matches 3; Conservative

||::| 1433 CHSIC 1437 1 CHAVC 5 g ઠે

Search completed: July 27, 2005, 00:02:32 Job time : 42 secs

hypothetical prote hypothetical prote alcohol dehydrogen triacylglycerol liprobable membrane protein F1086.14 (male-specific leth epidermal growth feromerved hypothet E2 glycoprotein pr E2 glycoproteic cystein hypothetical protein hypothetical protein probable oxidoreduxanthosine permeas xanthosine permeas

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Run

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T34728
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S64826
S64826
F86281
A27131
A27131
A27131
VGIHE3
VGIHE3
VGIHFS
S47423
VGIHFS
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A42125
B96981
T27516
QQEC30
D85934
B98089
G71343
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F72426
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                                                                   July 26, 2005, 23:51:45; Search time 39 Seconds (without alignments) 12.335 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                    protein search, using sw model
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MNXRPC

MNXRPC

MA44276

UYPVIM

UYPVIM

UYPVIM

UYPVIM

S09759

S34794

E86378

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Gapop 10.0 , Gapext 0.5
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34
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match 1
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                                                                                                                 Pitle:
Perfect score:
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Result Š.

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frizzled protein-2 hypothetical prote leukoriene B4 rec connexin40 - human alcohol dehydrogen hypothetical prote ZK66.4 protein -thyroid hormone re

transcription cont adenosylmethionine protein kinase Cds

vasopressin V3 rec

interferon-alpha -interferon-alpha -probable membrane hypothetical prote fumarate reductase

hypothetical prote L-rhamnose operon

us-10-632-678-10.rpr

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97.1%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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A, Note: T17J13.120
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                                                                                        RESULT 1

E84885

hypothetical protein At2g45010 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dates: 02-Feb-2001
G;Dates: 03-Feb-2001
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P27586; GB:M69115; NID:g333307; PIDN:AAA47087.1; PID:g333308
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNXRPC

MORETUCT 2

MORETUCTURAL protein NS34 - porcine rotavirus C (strain Cowden)

C;Species: porcine rotavirus C

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: A41040

R;Oian, Y, ; Jiang, B.; Saif, L.J.; Kang, S.Y.; Ojeh, C.K.; Green, K.Y.

Virology 184, 752-757, 1991

A;Title: Molecular analysis of the gene 6 from a porcine group C rotavirus that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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53563

Wypothetical protein - bovine rotavirus C
c;Species: bovine rotavirus C
c;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 535639
R;Jiang, B.; Tsunemitsu, H.; Gentsch, J.R.; Saif, L.J.; Glass, R.I.
Nucleic Acids Res. 21, 2250, 1993
A;Title: Nucleotide sequences of genes 6 and 10 of a bovine group C rotavirus.
A;Reference number: 535639; MUID:93275758; PMID:8389040
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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80.0%; Pred. No. 92;
.ive 1; Mismatches 0; Indels
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C;Superfamily: rotavirus nonstructural protein
C;Keywords: nonstructural protein
ALIGNMENTS
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nes 5; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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A,Gene: At2g45010
A,Map position: 2
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Pypothetical protein T17J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T48008
B;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, Psubmitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Reference number: Z24482
A;Reference number: Z24482
A;Residues: Proliminary
A;Residues: 1-428
A;Residues: 1-428
A;Residues: 1-428
A;Residues: 1-428
A;Resperimental source: cultivar Columbia; BAC clone T17J13
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    noncapeid protein NS1 - parvovirus LuIII
C;Species: A4276
R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-3145, 1993
A;Title: The complete nucleotide sequence of parvovirus LuIII and localization of a uniquence number: A44276
A;Title: The complete nucleotide sequence of parvovirus LuIII and localization of a uniquence number: A44276
A;Status: translation not shown
A;Status: translation not shown
A;Status: 1-668 vDIF>
A;Cross-references: UNIPROT:P36311; GB:M81888
C;Superfamily: parvovirus noncapsid protein
C;Superfamily: parvovirus noncapsid protein
A;Molecule type: DNA
A;Residues: 1-402 <JIA>
A;Residues: 1-402 <JIA>
A;Cross-references: UNIPROT:P34717; EMBL:L12390
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1993
C;Superfamily: rotavirus nonstructural protein
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Pred. No. 96;
1; Mismatches 0; Indels
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                                                                                                                                                                                                           2; Length 402;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                        97.1%; Score 33; DB
80.0%; Pred. No. 92;
live 1; Mismatches
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Gape

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Length 721;

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Richee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; R.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus Askeference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09903
A;Accession: S09903
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; notestine type; bun
A; Rossines 1-171 «CHB»
A; Rossines: 1-171 «CHB»
A; Rossines: 1-171 «CHB»
A; Cross-references: UNIPROT: P16808; EMBL: X17403; NID: 959591; PIDN: CAA35300.1; PID: 917809
A; Note: this sequence was submitted to the EMBL Data Library, December 1989
C; Keywords: 91ycoprotein; transmembrane prodein
C; Keywords: 91ycoprotein; transmembrane predicted 4SIG»
F; 26-171/Product: hypothetical protein IRL10 #status predicted 4MAT»
F; 70-103/Domain: transmembrane #status predicted <TWM»
F; 48, 49, 56, 108/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein TRL10 precursor - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence of human cytomegalovirus
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Status: nucleic acid sequence not shown content conten
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A;Molecule type: DNA
A;Residues: 1-171 <CHS
A;Cross-references: UNIPROT:Q69029; EMBL:X17403; NID:g59591; PIDN:CAA35458.1; PID:g59601
A;Cross-references: UNIPROT:Q69029; EMBL:X17403; NID:g59591; PIDN:CAA35458.1; PID:g59601
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Keywords: glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-171/Product: hypothetical protein TRLIO #status predicted <MAT>
F;70-103/Domain: transmembrane #status predicted <TWM>
F;48,49,56,108/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                        Score 33; DB 1; Le
Pred. No. 1.4e+02;
1; Mismatches 0;
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80.0%; Pred. No. 1.1e+02;
iive 1; Mismatches 0.
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A.Note: host Homo sapiens (man)
    C,Superfamily: parvovirus noncapsid protein C,Keywords: noncapsid protein
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Best Local Similarity 80.0%;
Matches 4; Conservative 1
                                                                                                                                97.1%;
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Best Local Similarity 80...
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Matches 4; Conservative
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CHAIC 431
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noncapsid protein NS1 - minute virus of mice (strain MVM1)

C; Species: minute virus of mice, murine parvovirus
C; Species: minute virus of mice, murine parvovirus
C; Species: minute virus of mice, murine parvovirus
C; Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C; Accession: A23008; A29510
R; Sahli, R:; McMaster, G.K.; Hirt, B.
Nucleic Acids Res. 13, 3617-3633, 1985
A; Till: DNA sequence comparison between two tissue-specific variants of the autonomous
A; Reference number: A23008; MUD: 85242059; PMID: 3855242
A; Recession: A23008
A; Molecule type: DNA
A; Residues: 1-721 < SAH>
A; Coss-references: UNIPROT: Q84363; EMBL: X02481
A; Ratell, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. S7, 656-669, 1986
A; Ratell, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. S7, 656-669, 1986
A; Reference number: A29510; MUD: 86115415; PMID: 3502703
A; Reference number: A29510
A; Residues: 1-645, I', 647-721 < AST>
A; Cross-references: EMBL: M12032; NID: 9332289; PIDN: AAA69566.1; PID: 93825477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outcome and protein NS1 - parvovirus H1
C;Species: parvovirus H1
C;Species: parvovirus H1
C;Species: parvovirus H1
C;Species: parvovirus H1
C;Accession: A03695
C;Accession: A03695
T;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybriatitle: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybriatitle: Parvovirus genome: nucleotide sequence of H-2 and mapping of its genes by hybriatitle: Parvovirus A03695
A;Reference number: A03695
A;Reference number: A03695
A;Residues: 1-672 < RHO>
A;Residues: 1-672 < RHO>
C;Superfamily: parvovirus noncapsid protein
C;Superfamily: parvovirus noncapsid protein
noncapsid protein NSI - minute virus of mice
C;Species: minute virus of mice, murine parvovirus
C;Date: 14-Nov-1983 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A03696
R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C.
Nucleic, Acids Res. 11, 999-1018, 1983
A;Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
A;Reference number: A03696; MUD:83143341; PMID:6298737
A;Residues: 1-672 <AST>
A;Residues: 1-672 <AST>
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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Pred. No. 1.38+02;
1; Mismatches 0; Indels
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Pred. No. 1.3e+02;
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conserv
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Length 171; 0; Indels ö

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A;Cross-references: UNIPROT:P07607; GB:M13352; NID:g202048; PIDN:AAA40444.1; PID:g202050 R;Perryman, S.M.; Rossana, C.; Deng, T.; Vanin, E.F.; Johnson, L.F. Mol. Biol. Brol. 3, 313-312, 1986 A;Fitcle: Sequence of a CDNA for mouse thymidylate synthase reveals striking similarity will A;Reference number: A24157; MUID:88174353; PMID:3444407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Rosidues: 1.307 <PER>
A,Rosidues: 1.307 <PER>
A,Rosidues: 1.307 <PER>
A,Crosidues: CS:M13019; NID:g202029; PIDN:AAA40439.1; PID:g202030
R,Crosidues: CS:M1019, L.F.
R,Deng, T.L.; Li, Y.; Johnson, L.F.
Nucleta Adida Res. 17, 645-658, 1989
A,Fitle: Thymidylate synthase gene expression is stimulated by some (but not all) introns
A,Reference number: 148858; MUID:89128436; PMID:2915925
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RjCiesla, J.; Weiner, K.X.B.; Weiner, R.S.; Reston, J.T.; Maley, G.F.; Maley, F.
Biochin. Biophys. Acta 1261, 233-242, 1995
A;Title: Isolation and expression of rat thymidylate synthase cDNA: phylogenetic comparite A;Reference number: S53715; MUID:95226450; PMID:7711067
A;Accession: S53715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-307 <CIE>
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                                                                                                    thymidylate synthase (EC 2.1.1.45) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 16-Aug-2004 C;Accession: A26323; A2167; 148858 R;Peng, T.; Li, D.; Jenh, C.H.; Johnson, L.F. J. Biol. Chem. 261, 16000-16005, 1986 A;Aritle: Structure of the gene for mouse thymidylate synthase. Locations of introns and A;Reference number: A26323; MUID:87087259; PMID:3782103
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
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A;Residues: 236-265 <RES>
A;Cross-references: EMBL:X14489; NID:954931; PIDN:CAA32651.1; PID:9899339
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80.0%; Pred. No. 1.7e+02;
iive 1; Mismatches 0; Indels
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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A;Status: translated from GB/EMBL/DDBJ
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80.0%;
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Matches 4; Conservative
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A;Residues: 1-307 <DEN>
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CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiAccession: E86378
CiAccession: E86378
CiAccession: E86378
CiAr. Coun, thung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
CiA.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Sowhey, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vonter, J.C.; Davis, R.W.
A;Title: Sequence and analyais of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                C;Species: Nıcotiana tabacum (common tobacco)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S34794; S37294
R;Singh, N.K.; Nelson, D.E.; Kuhn, D.; Hasegawa, P.M.; Bressan, R.A.
Plant Physiol. 90, 1096-1101, 1989
A;Title: Molecular cloning of osmotin and regulation of its expression by ABA and adapta
A;Reference number: S34794
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A;Cross-references: UNIPROT:Q9FYL9; GB:AE005172; NID:g9743332; PIDN:AAF97956.1; GSPDB:GN
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A; Map position: 1
C; Superfamily; Arabidopsis thaliana hypothetical protein F7A7.40; RING finger homology
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A;Residues: 1-128,'I',130-243 <SI2>
A;Cross-references: EMBL:M29279; NID:g170278; PIDN:AAA34089.1; PID:g170279
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A;Rebidues: 1.243 *SIN>
A;Cross-references: UNIPROT: P14170; EWBL: M29279
R;Singh, N.K.; Nelson, D.E.; Kuhn, D.; Hasegawa, P.M.; Bressan, R.A.
submitted to the EMBL Data Library, February 1990
A;Reference number: S17294
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80.0%; Pred. No. 1.4e+02;
iive 1; Mismatches 0; Indels
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Pred. No. 1.5e+02;
1; Mismatches 0;
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Local Similarity 80.0%;
les 4; Conservative
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                                                     CHAMC 64
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CHAVC 5
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A;Status: preliminary
A;Molecule type: DNA
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A; Status: preliminary
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RESULT 15

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Moeldues: 1-373 aVMCP.
A;Residues: 1-373 aVMCP.
A;Cross-references: UNIRROT: P91501; EMBL: UB8180; PIDN: AAB42300.1; GSPDB: GN00019; CESP: T2
A;Experimental source: strain Bristol N2; clone T27A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cjaccession: A69335
R;Klank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson R;Klank, H.P.; Clayton, R.A.; Tomb, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Mature 390, 364-370, 1997
Ajauthors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
Ajauthors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. AjTille: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo A; Reference number: A69250; MUID:98049343; PMID:9389475
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A;Cross-references: UNIPROT:029576; GB:AE001057; GB:AE000782; NID:g2689380; PIDN:AAB9055
C;Superfamily: Succinate dehydrogenase flavoprotein subunit; 3-oxosteroid 1-dehydrogenas
C;Keywords: FAD; flavoprotein; oxidoreductase
F;4-265/Domain: funarate reductase flavoprotein homology <PRF>
F;297-389/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>
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C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Species 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G87753
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G87753
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C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Introns: 80/1; 113/3; 154/2; 211/3; 273/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T27A3.7
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91.2%; Score 31; DB 2; Length 373
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
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                                                             R;Murray, J.; Wohldmann, P. submitted to the EMBL Data Library, February 1997 submitted to the EMBL Data Library, February 1997 A;Description: The sequence of C. elegans cosmid T27A3. A;Reference number: Z20110 A;Accession: T25920
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80.0%; Pred. No. 2.6e+02;
iive 1; Mismatches 0;
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les 4; Conserv
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A;Cross-references: GB:D00596; NID:g220135; PIDN:BAA00472.1; PID:g220136
B;Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotch, O.; Seno, T.
Biochem. 106, 575-583, 1999
A;Title: Human thymidylate synthase gene: isolation of phage clones which cover a functi A;Reference number: JU0120; MUID:90110051; PMID:2532645
A;Accession: JU0120
A;Status: translation not shown
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A, Residues: 1-313 «TAK»
A, Residues: 1-313 «TAK»
A, Cross-references: UNIPROT: P04818; EMBL: X02308; NID: 937478; PIDN: CAA26178.1; PID: 937479
R; Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.; Ayusawa,
R, Baol. Chem. 265; 2027-20284, 1990
A, Title: Structural and Functional Analysis of the Human Thymidylate Synthase Gene.
A, Reference number: 155318; MUID: 91056070; PMID: 2243092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Title: Purification and NH2-terminal amino acid sequence of human thymidylate synthase
Reference number: A22393; MUID:85261174; PMID:3839505
                                                                                                                                                                                                   thymidylate synthase (EC 2.1.1.45) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 16-Aug-2004
C;Accession: A23047; 155318; JU0120; A22393; A33842
R;Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.
Nucleic Acids Res. 13, 2035-2043, 1985
Nyrities: Nucleotide sequence of a functional cDNA for human thymidylate synthase.
A;Reference number: A23047; MUID:85215597; PMID:2987839
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A;Residues: 1-68 <TA2>
A;Crose-references: GB:D00517; NID:g220133; PIDN:BAA00404.1; PID:g2160415
R;Shimizu, K.; Ayusawa, D.; Takeishi, K.; Seno, T.
J. Biochem. 97, 845-850, 1985
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A;Residues: 2-25 <SH1>
R;Davisson, V.J.; Sirawaraporn, W.; Santi, D.V.
J. Biol. Chem. 26, 19145-9148, 1989
A;Title: Expression of human thymidylate synthase in Escherichia coli.
A;Reference number: A33842; MUID:89255401; PMID:2656695
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 80.0%
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A,Residues: 2-10 cDAV>
C,Genetics:
A,Gene: GDB:TYMS
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195 CHALC 199
                                           CHALC 193
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hypothetical protein T27A3.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

RESULT 16

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A,Cross-references: EMBL:XO6370; NID:g31118; PIDN:CAA29668.1; PID:g31119

B,Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1733, 1991

B,FHaley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1733, 1991

A,Title: Contributory effects of de Novo transcription and premature transcript termination a,R6672

A,Recession, A38672; MUID:91107677; PMID:1988448

A,Recession, A38672; MUID:91107677; PMID:1988448

A,Residues: 1-29 - HAL>
A,Cross-references: GB MM38425; MID:g181977; PIDN:AA63171.1; PID:g553271

A,Rober Conserreferences: GB MM38425; MID:g181977; PIDN:AA63171.1; PID:g553271

A,Experimental source: carcinoma cell line A431-7

B,Xu, Y; Ishii, S: Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Merl Nattle: Human epidernal growth factor receptor CDNA is homologous to a variety of RNAs c A; Title: Human epidernal growth factor receptor CDNA is homologous to a variety of RNAs c A; Reference number: A00642; MUID:84245835; PMID:6330563

A,Rocession A00642

A,Roberule type: mRNA
A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-321, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '798-799, '79
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A;Molecule type: mRNA
A;Residues: 1028-1210 < SIN>
Science 224, 294-297, 1984
A;Reference number: A05281; MUID:84172183; PMID:6324343
A;Accession: A05281
A;Molecule type: protein
A;Residues: 25-30, 'S', 32-51;454-467 < WEB>
B;Residues: 25-30, 'S', 32-51;454-467 < WEB>
A;Residues: 25-30, 'S', 32-51;454-467 < WEB>
A;Residues: 25-30, 'S', 32-51;454-467 < WEB>
A;Residues: 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleotide binding site of the epidermal growtherence number: A60143; MUID:85182650; PMID:2985580
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A, Molecule type: protein
A, Reseatches: 740-744, X', 746-747 < RUS>
A, Molecule type: protein
A, Reseatches: 740-744, X', 746-747 < RUS>
Nature 309, 270-273, 1984
A, Title: ATP-stimulated interaction between epidermal growth factor receptor and supercoff A, Title: ATP-stimulated interaction between epidermal growth factor receptor and supercoff A, Reference number: A38023, MUD: 84191554, PMID: 6325948
A, Roncents: annotation; receptor activity
A, Note: the BGF receptor (and other tyrosine kinases) can nick double-stranded DNA
A, Note: the BGF receptor (and other tyrosine kinases) can nick double-stranded DNA
A, Note: the BGF receptor (and other tyrosine kinases) can nick double-stranded DNA
A, Note: the BGF receptor (and other tyrosine kinases) can nick double-stranded DNA
A, Title: Functional independence of the epidermal growth factor receptor from a domain re
A, Reference number: A33331, MUDD: 9003233; PMID: 2790960
A, Title: Functional internalization signal
C, Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor constants.
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M. Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification of A;Reference number: $30024; MUID:88217333; PMID:3329716
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A,Across-references: GDB:120610, OMIM:131550
A,Kross-references: GDB:120610, OMIM:131550
A,Map position: 7p12.3-7p12.1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: autophosphorylation; duplication; glycoprotein; phosphomer
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-1210/Product: GGF receptor #status predicted <MAT>
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A; Residues: 713-964 <LIN>
A; Residues: 713-964 <LIN>
A; Experimental source: epidermoid carcinoma cell line A431
A; Experimental source: will, Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W. Biochem. Blophys. Res. Commun. 124, 125-132, 1984
A; Reference number: A23062; MUID:85046483; PMID:6093780
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A, Residues: 1-29 <HA2>
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Nature 309, 418-425, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of A;Reference number: A00641; MUID:84219729; PMID:6328312
A;Reference number: A00641
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1210 <ULL>
A;Cross-references: UNIPROT:P00533; EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g75792
A;Note: the authors translated the codon AAG for residue 540 as Asn
A;Note: the authors translated the codon AAG for residue 540 as Asn
A;Note: the authors translated the codon AAG for residue 540 as Asn
A;Note: the authors translated the solon AAG for residue 540 as Asn
A;Note: the cuthors translated the solon AAG for residue 540 as Asn
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A;Note: the cuthors translated the solon AAG for residue 540 as Asn
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A;Note: the cuthors translated the codon AAG for residue 540 as Asn
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                            A,Status: preliminary
A,Anolecule type: DNA
A,Anolecule type: DNA
A,Residues: 1-630 <870>
A,Cross-references: UNIPROT:P91149; GB:chr_I; PIDN:AAB37623.1; PID:g1703569; GSPDB:GN00C
C,Genetics:
A,Gene: C43B1.8
A,MAP position: 1
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Ksebidues: 1-111 <MIL>
A;Cross-references: UNIPROT:O9XWD6; EMBL:AL032657; PIDN:CAA21739.1; GSPDB:GN00019; CESP:
A;Experimental source: clone Y47H9C
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A,Map position: 1
A;Introns: 50/2: 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1083/1
C;Superfamily: ankyrin repeat homology; EGF homology
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C;Species: Caenorhabditis elegans
C;Species: Lact-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T26972
R;Harris, B.
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <ISH>
A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
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Pred. No. 2.8e+02;
1; Mismatches 0;
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Best Local Similarity 80.0
Matches 4; Conservative
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nes 4; Conservative
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284 CHAMC 288
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848 CHALC 852
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A;Cross-references: UNIPROT:045827; EMBL:Z82053; PIDN:CAB04832.1; GSPDB:GN00019; CESP:T2 A;Experimental source: clone T2653
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Akazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Experimental source: strain PCC 7120
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T2683.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25293
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60.0%; Pred. No. 1.2e+02;
tive 2; Migmatches 0;
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Pred. No. 1.2e+02;
0; Mismatches 1;
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Bubmitted to the EMBL Data Library, November 1996
A;Reference number: 220012
A;Accession: T25293
A;Accession: T25293
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Aclacule type: DNA
A;Residues: 1-106 <WIL>
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 3; Conserv
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CHSIC 15
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                                                                                                                                             21 CHCVC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHWC 57
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                                                    1 CHAVC 5
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A;Molecule type: DNA
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507
629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1
                                                                                                                                                                                                                                                                                                                                                                                                        F:1047-1210/Region: inhibitory
F:128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predic
F:745/Active site: Lys #status experimental
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C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999
C.Date: 2
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P;25-645/Domain: extracellular #status predicted <EXT>P;75-300/Domain: EGF receptor extracellular domain repeat <EE1>P;75-300/Domain: EGF receptor extracellular domain repeat <EE2>P;490-600/Domain: EGF receptor extracellular domain repeat <EE2>P;646-668/Domain: transmembrane #status predicted <ITMA>P;669-1210/Domain: intracellular #status predicted <INT>P;710-975/Domain: protein kinase homology <KIN>P;710-726/Region: protein kinase ATP-binding motif P;999-1046/Region: coated-pit mediated internalization signal
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91.2%; Score 31; DB 2; Length 2195;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%; Score 31; DB 1; Length 1210; 80.0%; Pred. No. 4.5e+02; ive 1; Mismatches 0; Indels
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Best Local Similarity 80.0
Matches 4; Conservative
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CHALC 510
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60.0%; Pred. No. 1.6e+02; ive 2; Mismatches 0
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60.0%;
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nes 3; Conservative
    Best Local Similarity 60.0
Matches 3; Conservative
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Matches 4; Conserv
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16 CHSIC 20
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95 CHSIC 99
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A; Introns: 41/1; 129/2
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                                                                          1 CHAVC 5
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Best Local S
Matches 3
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IVHOA1
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A;Modecule type: DNA
A;Residues: 1-154 <STO>
A;Cross-references: UNIPROT:Q8X758; GB:AE005174; NID:g12518866; PIDN:AAG59149.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yij1
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, & DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2543
A;Status: preliminary
A;Molecule type: DNA
A;Residcuse: 1-122 <KUR>
A;Cross-references: UMIPROT:Q82578; GB:AP003602; PIDN:BAB77277.1; PID:g17134719; GSPDB:GA;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A86086
hypothetical protein yijl [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A86086
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Axitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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E91238

hypothetical protein ECs4876 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91238

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence number: A99629; MUID:21156231; PMID:11258796
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                       Score 30; DB 2; Length 122;
Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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Best Local Similarity 60.0%;
Matches 3; Conservative ;
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-163 <HAY>
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CHSIC 29
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A,Gene: alr7634
A,Genome: plasmid
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interferon alpha-I-1 precursor - horse

NiAlternate names: EqIRN-alpha-I-1; type I interferon
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24912
R;Himmler, A: Hauptmann, R:; Adolf, G.R.; Swetly, P.
B;Himmler, A: Hauptmann, R:; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferor
A;Reference number: A30956; MUD:87053170; PMID:302299
A;Accession: A24912
A;Molecule type: DNA
A;Residues: 1-184
A;Molecule type: DNA
A;Crose-references: UNIPROT:P05003; GB:M14540; NID:g164226; PIDN:AA30953.1; PID:g164227
C;Superfamily: interferon alpha
C;Superfamily: interferon alpha
F;24-123/Domain: signal sequence #status predicted <NAT>
F;24-184/Product: interferon alpha-I-1 #status predicted
F;24-122,52-162/Disulfide bonds: #status predicted
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A;Experimental source: strain Bristol N2; clone M03F4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein M03F4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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R;Ful
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Pred. No. 1.7e+02;
2; Mismatches 0
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R;Edenberg, H.J.; Zhang, K.; Fong, K.; Bosron, W.F.; Li, T.K.
Proc. Natl. Acad. Sci. U.S.A. 82, 2262-2266, 1985
A;Title: Cloning and sequencing of cDNA encoding the complete mouse liver alcohol dehydr:
A;Reference number: A00338; WUID:85190477; PMID:3157987
                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M11307; NID:g191717; PIDN:AAA37180.1; PID:g309094
A;Note: in Genbank entry MUSADHIA, release 109.0, the source is designated as Mus caroli R;Caubin, J; Iglesias, T.; Bernal, J; Munoz, A.; Marquez, G.; Barbero, J.L.; Zaballos, Nucleic Acids Res. 22, 4132-4138, 1994
A;Title: Isolation of genomic DNA fragments corresponding to genes modulated in vivo by A;Reference number: S50102; MUID:95023181; PMID:7937138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:232540
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
R;Ceci, J.D.; Lawther, R.; Duester, G.; Hatfield, G.W.; Smith, M.; O'Malley, M.P.; Felde
R;Cene 41, 217-224, 1986
A;Title: Androgen induction of alcohol dehydrogenase in mouse kidney. Studies with a CDN
A;Reference number: A25849; MUID:86221702; PMID:3011597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triacylglycerol lipase (EC 3.1.1.3) 2 - Moraxella sp. (strain TA144)
C;Species: Moraxella sp.
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A39556
R;Feller, G.; Thiry, M.; Gerday, C.
DNA Call Bloil. 10, 381-388, 1991
A;Ttle: Nucleotide sequence of the lipase gene lip2 from the antarctic psychrotroph Mor A;Reference number: A39556; MUID:91321741; PMID:1907455
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A;Residues: 11433 <FEL>
A;Cross-references: UNIPROT:P24484; GB:X53868; NID:9296841; PIDN:CAA37862.1; PID:9296842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 224-375 <CB2>
; Cross-references: GB:M22611; NID:g191719; PIDN:AAA37181.1; PID:g191720
; Cross-references: GB:M22611; NID:g191719; PIDN:AAA37181.1; PID:g191720
; Comment: This enzyme converts primary and secondary alcohols to aldehydes using NAD as ; Comment: The active enzyme is a dimer of identical or nonidentical zinc-containing pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2

C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C; Superfamily: alcohol dehydrogenase; long-chaim; damer; metalloprotein; NAD;

C; Styperduct: alcohol dehydrogenase chain A; #status predicted «WAT>

F; 2-375/Product: alcohol dehydrogenase chain A; #status predicted «WAT>

F; 195-224/Region: beta-alpha-beta NAD nucleotide-binding fold

F; 196-224/Region: acceptated amino end (Ser) (in mature form) #status predicted

F; 7, Rodified site: alco, catalytic (Cys) #status predicted

F; 98, 101, 104, 112/Binding site: zinc, noncatalytic (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 3.2e+02;
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C,Keywords: carboxylic ester hydrolase
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                                                                      ;Cross-references: GB:M22611
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Best Local Similarity
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                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-375 < EDB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA;Residues: 8-51 <CAU>
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NiAlcernate names: alcohol dehydrogenase beta
NiAlcernate names: alcohol dehydrogenase beta
C;Species: Nus musculus (house mouse)
C;Date: 28-Feb-1986 #sequence revision 28-Feb-1986 #text_change 09-Jul-2004
C;Accession: A27322; A29628; Ā00338; S50103; A25849
K;Zbang, K; Bostron, W.F.; Edenberg, H.J.
A;Title: Structure of the mouse Adh-1 gene and identification of a deletion in a long al
C; Accession: T34728
R; Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Bubmitted to the EMBL Data Library, November 1998
A; Reference number: Z21555
A; Accession: T34728
A; Accession: T34728
A; Statuus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residuus: 1-319 <SEE>
A; Cross-references: UNIPROT: Q9ZC15; EMBL: AL033505; PIDN: CAA22035.1; GSPDB: GN00070; SCOED
A; Restimental source: strain A3(2)
C; Genetics: SCOEDB: SCIE6.07
C; Superfamily: Streptomyces coelicolor hypothetical protein SC4C6.19
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A; Residues: 1-372 <AQF>
A; Cross-references: UNIPROT: O67770; GB: AE000765; NID: 92984199; PIDN: AAC07741.1; PID: 9298
A; Experimental source: strain VF5
C; Genetics:
A; Gene: aq_1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein aq_1958 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70467
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A27322
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-375 <ZHA>
A;Cross-references: UNIPROT: P00329; GB:M11307; NID:g191717; PIDN:AAA37180.1; PID:g309094
B;Ceci, J.D.; Zheng, Y.W.; Felder, M.R.
Gene 59, 171-182, 1987
A;Title: Molecular analysis of mouse alcohol dehydrogenase: nucleotide sequence of the A;Reference number: A29628; MUID:88137953; PMID:2893758
A;Accession: A29628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 192, 153-158, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Acesence number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70467
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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Pred. No. 2.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.2%; Score 30; DB 2; Length 319;
80.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 1; Indels
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A,Reference number: A27322, MUID:88112859, PMID:3428612
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male-specific lethal 2 protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55554
E;Abou, S.; Yang, Y.; Scott, M.J.; Pannuti, A.; Fehr, K.C.; Eisen, A.; Koonin, E.V.; Fout-18120 J. 14, 2884-2895, 1995
A;Title: Malle-specific lethal 2, a dosage compensation gene of Drosophila, undergoes sex-A;Reference number: S55554; MUID:95317307; PMID:7796814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-769 <ZHO>
A;Cross-references: UNIPROT:P50534; EMBL:Z48443; NID:g872110; PIDN:CAA88358.1; PID:g872111
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Drosophila melanogater
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A27131
R;Schejter, E.D; Segal, D.; Glazer, L.; Shilo, B.Z.
Cell 46, 1091-1101, 1986
A;Title: Alternative 5' exons and tissue-specific expression of the Drosophila EGF recept: A;Reference number: A27131; MUID:87002474; PMID:3093080
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B81704
conserved hypothetical protein TC0424 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Bate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermal growth factor receptor - fruit fly (Drosophila melanogaster) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A;Molecule type: mRNA
A;Residues: 1-843 <SCH>
A;Cross-references: UNIPROT:QBMLW0
C;Genetics:
A;Gene: FlyBase:Bgfr
A;Cross-references: FlyBase:FBgn0003731
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
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80.0%; Pred. No. 5.2e+02;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 769;
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Pred. No. 4.8e+02;
0; Mismatches 1;
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A;Cross-references: FlyBase:FBgn0005616
A;Introns: 641/1
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                   464 CHAAC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 CHCVC 556
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                           1 CHAVC 5
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R; Vandenbol, M; Portecelle, D.; Hilger, F.

submitted to the Protein Sequence Database, May 1996

A; Reference number: 564742

A; Accession: 564742

A; Accession: 56472

A; Accession: 564742

A; Residues: 1-523 < VAN>
A; Residues: 1-523 < VAN>
A; Cross-references: UNIPROT: Q07904; EMBL: Z73176; NID: G1360291; PID: e245487; PID: g1360292
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein F10B6.14 [imported] - Arabidopsis thaliana cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86281
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., i.i., J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Roway, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: F86581
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C; Genetics:
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                                                                                                                                                                                                                                                                    probable membrane protein YLR004c - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein L1515
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
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   Gaps
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Pred. No. 4.8e+02;
0; Mismatches 1; Indels
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;242-258/Domain: transmembrane #status predicted <TM4> F;342-261/Domain: transmembrane #status predicted <TM5-F;379-395/Domain: transmembrane #status predicted <TM6F;467-483/Domain: transmembrane #status predicted <TM6F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;123-139/Domain: transmembrane #status predicted <TM2>F;147-163/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: transmembrane protein;78-94/Domain: transmembrane #status predicted
   Mismatches
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80.0%;
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A,Cross-references: SGD:S0003994
A,Map position: 12R
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   4; Conservative
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Best Local Similarity
Matches 4; Conserva'
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-760 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 CHAAC 165
                                                                                                                     181 CHTVC 185
                                                          1 CHAVC 5
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Gene: F10B6.14
   Matches
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A;Residues: 1434-1447 <RAW>
A;Cross-references: EMBL:X06371
A;Cross-references: EMBL:X06371
A;Experimental source: strain Purdue-115
C;Superfamily: coronavirus E2 glycoprotein
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane predicted <SIG>
F;1-16/Domain: signal sequence #status predicted <MAT>
F;1387-1431/Domain: transmembrane #status predicted <MM>
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91
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A;Note: the authors translated the codon GAA for residue 388 as Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1391-1411/Domain: transmembrane #status predicted <TMN>
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84
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E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain FS772/7)

E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain FS772/7)

N.Alternate names: peplomer glycoprotein, spike glycoprotein

C.Species: porcine transmissible gastroenteritis virus

C.Species: 30-Jun-1993 agequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C.Accession: B43489; S11728

F. Britton, P.; Page, K. W.

Virus Res. 18, 71-80, 1990

A;Title: Sequence of the S gene from a virulent British field isolate of transmissible contraction number: A43489; MUID:91188698; PMID:1964522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastroenteritis virus (strain Miller)
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A,Realdues: 1-1449 eMR>
A,Realdues: 1-1449 eMR>
A,Cross-references: UNIRROT:P18450, GB:X53128; NID:g61377; PIDN:CAA37285.1; PID:g61379
C,Superfamily: coronavirus E2 glycoprotein
C,Reywords: glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1449/Product: E2 glycoprotein #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Milla N; Alternate names: peplomer glycoprotein; spike glycoprotein C; Species: porcine transmissible gastroenteritis virus C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C; Accession: A43573 R; Wesley, R.D. A3575 A30-306, 1990 A4V. Exp. Med. Biol. 276, 301-306, 1990 A; Title: Nucleotide sequence of the E2-peplomer protein gene and partial nucleotide shiftle: Nucleotide sequence of the R2-peplomer protein gene and partial nucleotide shiftle: Nucleotide sequence muchor: A43573; MUID: 91353366; PMID:1966416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1449;
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C;Keywords: glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>
F;1027-1043/Region: hydrophobic
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Pred. No. 7.6e+02;
2; Mismatches 0
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Pred. No. 7.6e+02;
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60.0%;
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60.0%;
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Best Local Similarity 60...
3; Conservative
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Best Local Similarity 60.v
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A; Residues: 1-1449 <WES>
                           A; Molecule type: genomic RNA
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1426 CHSIC 1430
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VGIHE2
B2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Purdue-1
N;Alternate names: spike glycoprotein
C;Species: porcine transmissible gastroenteritis virus
A;Variety: strain Purdue-115
C;Bate: 31-6-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A27106; S01738
C;Accession: A27106; S01738
R;Rasschaert, D.; Laude, H.
J. Gen. Virol. 68, 1883-1890, 1987
A;Title: The predicted primary structure of the peplomer protein E2 of the porcine coron
A;Reference number: A27106; MUID:87253116; PMID:3037011
A;Residues: 1-1447 cRAS>
A;Residues: 1-1457 cRAS>
A;Residues: 1-165 CSD15000 CSD18000 CSD18000 CSD18000 CANDA CA29175.1; FA;Rasschaert, D.; Gelfi, J.; Laude, H.
Biochimie 69, 591-600, 1987
A;Title: Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization
A;Reference number: S01738; MUID:88078100; PMID:2825819
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: B81704
A;Accession: B81704
A;Accession: B1704
A;Accession: B1704
A;Accession: B1704
A;Residues: J-1436 <TET>
A;Cross-references: UNIPROT:09PKP1; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3928
A;Cross-references: train Nigg (MoPn)
C;Genetics:
A;Gene: TC0424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGIHE3

E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Purdue)

M;Alternate names ipeplomer protein; spike glycoprotein

G;Species bordine transmissible gastroenteritis virus

C;Species porcine transmissible gastroenteritis virus

C;Date: 30-Uun-1990 #sequence_revision 30-Uun-1990 #text_change 12-Apr-1996

C;Accession: JS0336

G;Accession: JS0336

K;Jacobs, L.; de Groot, R.; van der Zeijst, B.A.M.; Horzinek, M.C.; Spaan, W.

Virus Res. 8, 363-371, 1987

A;Title: The nucleotide sequence of the peplomer gene of porcine transmissible gastroent

g (FIPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1447 <JAC>
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane predicted <SIG>
F;1-16/Domain: signal sequence #status predicted <SIG>
F;1-1447/Product: E2 glycoprotein #status predicted <MMT>
F;1387-1431/Domain: transmembrane #status predicted <TMM>
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: JS0336; MUID:88129049; PMID:2829461
A;Accession: JS0336
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 2; 1
Pred. No. 7.6e+02;
0; Mismatches 1;
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60.0%; Pred. No. 7.6e+02;
ive 2; Mismatches 0
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80.0%;
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1426 CHSIC 1430
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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C;Accession: A27771
R;De Groot, R.J.; Maduro, J.; Lenstra, J.A.; Horzinek, M.C.; Van Der Zeijst, B.A.M.; Spaa
J.Gen. Virol. 68, 2639-2646, 1987
A;Title: cDNA cloning and sequence analysis of the gene encoding the peplomer protein of
A;Reference number: A27171; MUID:88034948; PMID:3312491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A27111
A;Molecule type: genomic RNA
A;Residues: 1-1452 <-DEG>
A;Residues: UNIPROT: P10033; GB:X06170; GB:D00150; NID:g58915; PIDN:CAA29535.1; Pl)
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; ransmembrane predicted <-SIG>
F;1-19/Domain: signal sequence #status predicted <-Mil>
F;1-19/Domain: transmembrane #status predicted <-TML>
F;1-19/Product: spike glycoprotein #status predicted <-TML>
F;134-1414/Domain: transmembrane #status predicted <-TML>
F;139-1414/Domain: transmembrane #status predicted <-TML>
F;29,95,174,208,234,241,288,337,348,365,408,452,483,519,535,557,565,707,728,783,822,837,8
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C'Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C'Accession: 31453
R;Wesseling, J.G.; Vennema, H.; Godeke, G.J.; Spaan, W.J.M.; Horzinek, M.C.; Rottier, P.:
submitted to the EMBL Data Library, December 1993
A;Bescription: Nucleotide sequence and expression of the spike (S) gene of canine coronav
A;Reference number: $41453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1453 <WES>
A/Cross-references: UNIPROT: Q65984; EMBL: X77047; NID: G452379; PIDN: CAAS4335.1; PID: G45235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2 glycoprotein precursor - feline infectious peritonitis virus (strain 79-1146) N;Alternate names: peplomer glycoprotein; spike glycoprotein C;Species: feline infectious peritonitis virus C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
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                                Length 1451;
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Pred. No. 7.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IndelB
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                            Score 30; DB 1;
Pred. No. 7.6e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: coronavirus E2 glycoprotein
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                                88.2%;
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60.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                              3; Conservative
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1430 CHSIC 1434
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                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                      1 CHAVC 5
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Matches
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JO1719
E.2 glycoprotein precursor - canine coronavirus (strain Insavc-1)
N.Alternate names: spike glycoprotein
C.Species: canine coronavirus
C.Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C.Accession: 407119
R.HOrsburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A.Jille: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNP A.Reference number: PQ0481; MUD:93057357; PMID:1431811
A.Accession: JQ1719
A.Accession: JQ1719
A.Residues: 1-1451 - AHOR.
A.Residues: 1-1451 - AHOR.
A.Residues: UNIPROT:P36300; DDBJ:D13096; NID:g406193; PIDN:BAA02408.1; PID:g4061
C.Gene: C.Gene: C.G.Gene: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
547423
E2 91ycoprotein precursor - porcine transmissible gastroenteritis virus
E2 91ycoprotein precursor - porcine transmissible gastroenteritis virus
E2 91ycoprotein precursor - porcine transmissible gastroenteritis virus
E2,5peties: 23-Nov-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C3Accession: 865851, 847423
C3Accession: 865851, 847423
E3 18 1999, 1995
B3 1999, 1999, 1995
A3 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999, 1999,
F;1027-1043/Region: hydrophobic
F;1395-1411/Domain: transmembrane #status predicted <TMN>
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84
d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1449 <CH2>
A;Cross-references: UNIPROT:Q88510; EMBL:235758; NID:9529246; PIDN:CAA84806.1; PID:e
A;Experimental source: Taiwanese field isolate
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                            Length 1449;
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60.0%; Pred. No. 7.6e+02;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
E;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>
                                                                                                                                                                                                                                                            Score 30; DB 1; I
Pred. No. 7.6e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                88.2%;
60.0%;
                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Pest Jone 3; Conservative
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1428 CHSIC 1432
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es 3; Conserv
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A, Residues: 1-120 <WIL>
A, Cross-references: UNIPROT:Q9XUI8; EMBL:Z82082; PIDN:CAB04963.1; GSPDB:GN00019; CESP:ZC
A, Experimental source: clone ZC334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 31-Mar-1988 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: B65065; C2137
R; Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-187 - SBLAT>
A;Residues: 1-187 - SBLAT>
A;Residues: 1-187 - SBLAT>
A;Experimental source: strain K-12, substrain MG1655
R;Finch, P.W.; Wilson, R.B.; Brown, K.; Hickson, I.D.; Tomkinson, A.E.; Emmerson, P.T.
Nucleic Acids Res. 14, 4437-4451, 1986
A;Title: Complete nucleotide sequence of the Escherichia coli recC gene and of the thyA-A;Reference number: A93625; MUID:86232583; PMID:3520484
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;Cross-references: GB:X03966; NID:g42684; PIDN:CAA27601.1; PID:g42686
                                                                                                                                                                                                                hypothetical protein ZC334.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Acession: T27516
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C;Superfamily: prepilin peptidase dependent protein B precursor
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Pred. No. 2.6e+02;
1; Mismatches 1;
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Pred. No. 1.9e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November 1996
A;Reference number: 220381
A;Accession: T27316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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hes 3, Conserv
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Best Local Similarity
Matches 3; Conserv
                              1 CHAVC 5
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21 CHCIC 25
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CHGIC 72
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A; Map position: 1
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Best Local S
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B96981
hypothetical protein CAC0660 [imported] - Cloatridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B96981
R;Nolling, J; Breton, G; Omelchenko, M.V; Markarova, K.S; Zeng, Q; Gibson, R.; Lee,
J; Baly, M.J; Bennett, G;N; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96981
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-67 cKUR>
A;Cross-references: UNIPROT:Q97LA2; GB:AE001437; PIDN:AAK78637.1; PID:g15023535; GSPDB:C
C;Genetics: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene: CAC0660
                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1269-1766 <ADA2>
A, Residues: 1269-1766 <ADA2>
A, Residues: 1269-1766 <ADA2>
A, Cross-references: GB.M83933; NID:g159122
A, Cross-references: GB.M83933; NID:g159122
A, Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is nc R, Adam, R.D.; Aggarwal, A.J. Lal, A.A.; de la Cruz, V.F.; McCutchan, T.; Nash, T.E.
J. Exp. Med. 167, 109-118, 1988
A, fitle: Antigenic variation of a cysteine-rich protein in Giardia lamblia.
A, Reference number: S00530; MUID:88089405; PMID:3335828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>
A; Cross-references: EMBL:X06741; NID:g9355; PID:g929603
R; Yang, Y.; Adam, R.D.
Nucleic Acide Res. 22, 2102-2108, 1994
A; Title: Allele-specific expression of a variant-specific surface protein (VSP) of Giard
A; Reference number: $48056; MUD:94301794; PMID:8029018
                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-98 aCAD1-
A; Residues: 1-98 aCAD1-
A; Residues: 1-98 aCAD1-
A; Experimental source: trophozoite
A; Experimental source: trophozoite
A; Note: sequence extracted from NCBI backbone (NCBIN:88421, NCBIP:88427); this ORF is nc
A; Note: the authors report but do not show 19 tandem repeats of the sequence of residues
A; Accession: 842125
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: A42125; B42125; $50530; $48056
C;Accession: A42125; B42125; Z00530; $48056
Mol. Cell. B101. 12, 1194-1201, 1992
A;Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 generated number: A42125; MUID:92186850; PMID:1545800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: trophozoites WBA6
A;Note: the source is designated as Giardia intestinalis
C;Comment: This translation was produced by PIR staff from information provided by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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A,Residues: 1-56 <YAN>
A,Cross-references: EMBL:L25059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 80.0
المالية 4. Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-219 <COL>
A;Cross-references: UNIPROT: 083308; GB:AE001209; GB:AE000520; NID:g3322547; PIDN:AAC6528(
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CiAccession: M82147

Rifeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

I, R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: A82147

A;Status: preliminary

A;Rolecule type: DNA

A;Residues: 1-228 chEL>

A;Residues: 1-228 chEL>

A;Resperimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:057208; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA1019-A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: Mg2+-transporting ATPase
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 876342
R; Kaneko, T: 5ato, S:; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC transporter, ATP-binding protein VC1883 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: VC1883
A;Map position: 1
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                     Length 219;
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85.3%; Score 29; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                           A;Gene: TP0284
C;Superfamily: syphilis spirochete hypothetical protein TP0284
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A;Accession: S76342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <KAN>
                                                                                                                                                                                                                                                                                                                                                                  Query Match
85.3%; Score 29; DB 2; I
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1;
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Bagaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. B, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genchy a; Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B9808

A;Accession: B9808

A;Accession: B9808

A;Molecule type: DNA

A;Molecule type: DNA

A;Residuae: 1-187 cHAY>

A;Cross-references: UNIPROT:QBX6M2; GB:BA000007; PIDN:BAB37105.1; PID:gl3363154; GSPDB:CA

A;Experimental source: strain O157:H7, substrain RIMD 0509952
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G71343

G71343

C) Proportion of the protein TP0284 - syphilis spirochete

C) Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C) Species: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C) Accession: G71343

R) Fraser. C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinren, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDdrien, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:QBX6M2; GB:AE005174; NID:g12517310; PIDN:AAG57936.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                      prepilin peptidase dependent protein B [imported] - Escherichia coli (strain O157:H7, su C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
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A;Gene: ECe3582
C;Superfamily: prepilin peptidase dependent protein B precursor
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C;Superfamily: prepilin peptidase dependent protein B precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Status: preliminary
A Molecule type: DNA
A;Residues: 1-187 <STO>
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CHGIC 72
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68 CHGIC 72
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C)Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C)Accession: 140700; 837179
C;Accession: 140700; 837179
C;Accession: 140700; 837179
C;Accession: 140700; 837179
A;Title: Cloning and analysis of translational control for genes encoding the Cfr91 rest A;Reference number: 140699; MUID:94215893; PMID:8163180
A;Accession: 140700
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Accession: DNA
A;Acce
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A;Cross-references: UNIPROT:Q60132; EMBL:X74517; NID:g402178; PIDN:CAA52628.1; PID:g4021
C;Genetics:
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Cispecies: Methanococcus Jannaschii
Cispecies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
CiAccession: A64378
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Reich, C.I.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Tille: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q58042; GB:U67510; GB:L77117; NID:g1591325; PIDN:AAB98625.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type II site-specific deoxyribonuclease (BC 3.1.21.4) Cfr9I - Citrobacter freundii
C;Species: Citrobacter freundii
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A;Molecule type: DNA
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A;Experimental source: cultivar Columbia
C;Genetics:
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85.3%; Score 29; DB 2; Length 336;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 3; Conservative 1; Mismatches 1; Indels
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Pred. No. 3.7e+02;
1; Mismatches 1;
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85.3%; Score 29; DB 2; I
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1;
                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
submitted to the EMBL Data Library, September 1999
A;Reference number: 226062
A;Accession: T52387
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C;Superfamily: ATP-binding protein PAB1945
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Best Local Similarity 60...
Best Local 3; Conservative
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                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-307 < KAN>
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41 CHGIC 45
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C,Keywords: hydrolase
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A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A,Reference number: A72200; MUD:99287316; PMID:10360571

A,Reference number: A72200; MUD:99287316; PMID:10360571

A,Residue: Preliminary
A,Residues: preliminary
A,Residues: 1-261 cARN>
A,Residues: 1-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iron-sulfur cluster-binding protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11.-Uun-1999 #sequence_revision 11.-Uun-1999 #text_change 16-Aug-2004
C;Accession: F72426
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.:
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hypothetical protein al41L - Chlorella virus PBCV-1
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T17632
R; Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A; Reference number: 218806
A; Reference number: z18806
A; Reference number; translated from GB/EMBL/DDBJ
A; Residues: 1-265 <GRA>
A; Residues: 1-265 <GRA>
A; Residues: 1-265 <GRA>
A; Cross-references: UNIPROT: Q84461; EMBL: U42580; NID: G4028896; PIDN: AAC96509.1
A; Experimental source: specific host Chlorella strain NC64A
C; Genetics:
A; Note: a141L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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80.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 1; Indels
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Pred. No. 3.4e+02;
1; Mismatches 1; Indels
                                                                    1; Indels
                   80.0%; Pred. No. 3.1e+02; ive 0; Mismatches 1
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C,Superfamily: ferredoxin 2[4Fe-4S] homology
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Best Local Similarity 60.0
Matches 3; Conservative
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Matches 4; Conservative
                                                                    4; Conservative
              Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                   149 CHLVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHAVC 5
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                                                                                                                                                            1 CHAVC 5
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Cipecies: Methanococcus januaschii
Cipate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
Cipate: 13-Sep-1996 #sequence_revision 15-Sep-1996 #text_change 09-Jul-2004
R;Bult, C.J; White, O.; Olsen, G.J; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, L.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1956
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A;Reference mumber: A64300; MUID:96337999; PMID:8688087
A;Reference mumber: A64405
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-359 *cBUL.
A;Cross-references: UNIPROT:Q58412; GB:U67543; GB:L77117; NID:g1591663; PIDN:AAB99014.1; C;Genetics:
A;Map position: FOR934363-935442
A;Statt codon: TTG
C;Superfamily: AIP-binding protein PAB1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DaBoy, K.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H8734
A;Accession: H8734
A;Adolecule type: DNA
A;Residues: 1-380 <STO>
A;Cross-references: UNIPROT:Q9AA37; GB:AE005673; NID:g13422010; PIDN:AAK22756.1; GSPDB:GA
C;Genetics:
A;Genetics:
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Psep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathoma; Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 4.2e+02;
1; Mismatches 1; Indels
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80.0%; Pred. No. 4.3e+02;
ive 0; Mismatches 1; Indels
hypothetical protein MJ1006 - Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.3%;
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Matches 3; Conservative
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 CHVIC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHAVC 5
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                                                                                                                                                                                                                                                      hypothetical protein MJ1076 - Methanococcus jannaschii

Cispecies Mitte, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Rebut, C.J.; White, O.; Olsen, M. J.; Zhou, L.; Fleischmann, R.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Thile: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: C64434

A;Accession: C64434

A;Residues: 1-337 < BUL.>

A;Molecule type: DNA

A;Residues: 1-337 < BUL.>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hoffs13
hypothetical protein MJECL26 - Methanococcus jannaschii plasmid pURB800
C;Species: Methanococcus jannaschii na. Sep-1996 #text_change 09-Jul-2004
C;Species: Mathanococcus jannaschii na. Sep-1996 #text_change 09-Jul-2004
C;Baccession: A64513
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; Overbeek, R.; Kirkness, B.F.; Wainstock, K.G.; Merrick, J.M.; Glodek, A.; Eson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A; Itle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii ArReference number: A64300; MUID:96337999; PMID:8688087
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A;Genome: plasmid
A;Start codon: TTG
A;Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromoso
C;Superfamily: ATP-binding protein PAB1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: Q58476; GB: U67550; GB: L77117; NID: g1591722; PIDN: AAB99081.1; C; Genetics:
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-343 <BUL>
A;Cross-references: UNIPROT:Q60285; GB:L77118; NID:g1500644; TIGR:MJECL26; PIDN:AAC37097
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60.0%; Pred. No. 4e+02;
ive 1; Mismatches
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C;Superfamily: ATP-binding protein PAB1945
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CHVIC 172
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168 CHVIC 172
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172 CHVIC 176
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                                          CHAVC 5
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C;Accession: T52320
R;Walker, K.; Croteau, R.
Proof. J. Acad. Sci. U.S.A. 97, 583-587, 2000
A;Title: Molecular cloning of a 10-deacetylbaccatin III-10-0-acetyl transferase cDNA from A;Reference number: Z26035
A;Accession: T52320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypochetical protein F2187.32 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00918
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Consultant, P.; EMBL Data Library, January 1998
A;Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A;Reference number: 214208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-461 <SHI>
A;Cross-references: UNIPROT:Q9LR83; EMBL:AC002560; NID:G2618677; PID:G2809263; GSPDB:GNO
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                                                                                                                                                              10-deacetylbaccatin III-10-0-acetyl transferase [imported] - Taxus cuspidata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F07A5.3 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Saccession: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C.Accession: T20537 R.Wilkinson, J. Bubmitted to the EMBL Data Library, May 1996 A.Reference number: 219288 A.Reference number: 219288
                                                                                                                                                                                                              C;Species: Taxus cuspidata
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-440 <WAL>
A;Cross-references: UNIFROT:Q9MGE2; EMBL:AF193765; PIDN:AAF27621.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 440;
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60.0%; Pred. No. 4.8e+02;
iive 1; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-590 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.3%; Score 29; DB 2;
60.0%; Pred. No. 5e+02;
ive 1; Mismatches
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Best Local Similarity 60.0
Matches 3; Conservative
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nes 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHGIC 165
75 CHLVC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: T00918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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AC0809
xanthosine permease [imported] - Salmonella enterica subsp. enterica serovar Typhi (stractions)
xanthosine permease [imported] - Salmonella enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001
A;Note: 09-Nov-2001
C;Accession: AC0809
R;Perkhill. J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
C, S.; Moule, S.; O'Gaora, D.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <PRA>
A;Residues: 1-418 <PRA>
A;Residues: 1-418 <PRA>
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escolut
C;Species: Escolut
C;Accession: Escolut
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1455-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Attle: The complete genome sequence not shown; translation not shown
A;Rolecule type: DNA
A;Residues: 1-418 <BLAT>
A;Residues: 1-418 <BLAT>
A;Residues: 1-418 <BLAT>
A;Residues: 1-418 <BLAT>
A;Reperimental source: strain K-12, substrain MG1655
C;Genetics:
A;Genetics:
A;Geneti
A;Molecule type: DNA
A;Residues: 1-416 <STO>
A;Cross-references: UNIPROT:Q9HU99; GB:AE004921; GB:AE004091; NID:g9951372; PIDN:AAG0846
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA5084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 418;
                                                                                                                                                                                                                                               Score 29; DB 2; Length 416;
Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
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                                                                                                                                                                                                                                           85.3%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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C;Accession: T39715
R;Beck, A; Reinhardt, R; Wood, V; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, September 1998
A;Reference number: Z21872
A;Recession: T39715
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:O74759; EMBL:AL031739; PIDN:CAA21075.1; GSPDB:GN00067; SPDB:&A;Experimental source: strain 972h-; cosmid c17D11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cispecies: Arar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hughes, B.; Huizar, L.
Antere 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, E. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, E. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription regulator, phd finger protein - fission yeast (Schizosaccharomyces C,Species: Schizosaccharomyces pombe C,Date: 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-references: UNIPROT: Q9LP09; GB: AE005173; NID: g8778679; PIDN: AAF79687.1; GSPDB: GNL
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                    A;Gene: CESP:F09B9.1
A;Map position: A
A;Introns: 82/1: 196/2: 379/1; 626/3; 655/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F09B9.1
                                                                                                                                                                                                                                                               Score 29, DB 2; Length 710;
Pred. No. 6.8e+02;
0; Mismatches 1; Indels
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Pred. No. 7.2e+02;
1; Mismatches 1; Indels
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Pred. No. 8.3e+02;
0; Mismatches 1; Indels
    A; Experimental source: clone F09B9
                                                                                                                                                                                                                                                                       85.3%;
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                                                                                                                                                                                                                                                               Query Match 85.3
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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270 CHTIC 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CHAVC 5
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                                    C, Genetics
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T20635
Hypothetical protein F09B9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20635
R;Kerence number: Z19303
A;Reference number: Z19303
A;Accession: T20635
A;Accession: T20635
A;Accession: Preliminary; translated from GB/EMBL/DDBJ
A;Accession: J-10 eWIL>
A;Accession: J-710 eWIL>
A;Accession: BNA
A;Accession: BNA
A;Coss-references: UNIPROT:019239; EMBL:Z49887; PIDN:CAA90058.1; GSPDB:GN00028; CESP:FG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    follitropin receptor precursor - newt

N.Alternate names: follicle-stimulating hormone receptor

C;Alternate names: follicle-stimulating hormone receptor

C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C;Date: 17-Nov-2000

R;Accession: JC7361

R;Nakayama, Y: Y Amamoto, T.; Oba, Y: Nagahama, Y:; Abe, S.

Biochem. Biophys. Res. Commun. 275, 121-128, 2000

A;Title: Molecular cloning, functional characterization, and gene exppression of a folling A;Contents: Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mNAA A;Residues: 1-696 <NAK>
A;Residues: 1-696 <NAK>
A;Cross-references: UNIPROT:Q9DGF5; DDBJ:AB005587
C;Comment: This protein, containing seven transmembrane domains and a large glycosylated in and thyroid stimulating hormone. This receptor has a common signal transduction pathw C;Genetics:
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Cisuperfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat H
Cisuperfamily: glycoprotein processes and sequence #status glycoprotein; hormone receptor; testis; transmem
Fil-17/Domain: signal sequence #status predicted <SIG>
Fil-18-55/Domain: extracellular #status predicted <EXT>
Fil-18-55/Domain: extracellular #status predicted <EXT>
Fil-18-55/Domain: transmembrane #status predicted <TMI>
Fil-18-55/Domain: transmembrane #status pr
A;Experimental source: clone F07A5
C;Genetics:
A;Gene: CESP:F07A5.3
A;Map position: 1
A;Introns: 42/3; 101/2; 151/3; 185/2; 208/3; 240/3; 290/1; 333/2; 370/2; 462/3; 487/2
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80.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 1; Indels
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Pred. No. 6.7e+02;
0; Mismatches 1
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Best Local Similarity 80.0<sup>,</sup>
"Then 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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A; Cross-references: UNIPROT: 077360; EMBL: AL008970; NID: e1407852; PID: e1332566; PIDN: CAA1
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R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1737 < KNA
A;Residues: 1-1737 < KNA
A;CEGE TEEFER EMBL, AB011541; NID:93449307; PIDN:BAA32469.1; PID:93449308
A;Experimental source: brain; clone HG1392
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C;Species: Schizosaccharomyces.pombe
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C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (mān)
;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
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60.0%; Pred. No. 1.6e+03;
iive 1; Mismatches 1;
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Pred. No. 1.3e+03;
0; Mismatches 1;
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Pred. No. 1.1e+03;
0; Mismatches 1;
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submitted to the EMBL Data Library, November 1998
A;Reference number: 218937
A;Accession T18472
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2269 <LAW>
C; Keywords: ATP; phosphotransferase P;707-972/Domain: protein kinase homology <KIN>P;715-723/Region: protein kinase ATP-binding motif
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Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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T38057
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A; Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
C; Genetics:
A; Gene: GDB:ERBB3; HER3
A; Cross-references: GDB:119880; OMIM:190151
A; Map position: 12g13-12g13
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cossides: 1-1342 <KRNA
A;Cross-references: UNIPROT: P21860; GB:M29366
A;Cross-references: UNIPROT: P21860; GB:M:G.; Green, J.M.; McDonald, V.L.; Todaro, G.J.
B;Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J.
A;Ptole: Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor-re
A;Reference number: 159164; MUID:90311312; PMID:2164210
A;Accession: I59164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Residues: 1-1339 <HEL>
A)Cross-references: GB:U29339; NID:g915389; PID:g915390
A)Cross-references: GB:U29339; NID:g915389; PID:g915390
A)Experimental source: liver
A)Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue C;Comment: This protein is a functional heregulin receptor that transduces signals to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ੁ
                                                                                                                                                                                                                                                                                   Jog4387

Spidermal growth factor receptor homolog precursor - rat
NyAlternate names: ErbB3 protein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
C;Accession: JG4387
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.
A;Reference number: JG4387; MUID:96096535; PMID:8522190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 76

kinage-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human

kjaces Homo sapiens (man)

Cjoedes: Homo sapiens (man)

Rjaces 
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F;713-721/Region: protein kinase ATP-binding motif
F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding site: phosphate (Tyr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: protein kinase homology
C; Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1339/Porduct: epidermal growth factor homolog #status predicted <MAT>
F;640-659/Domain: transmembrane #status predicted <TWM>
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A,Molecule type: mRNA
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Best Local Similarity
Matches 4; Conserv
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A,Cross-references: UNIPROT:097945; GB:M28626; NID:g163977; PIDN:AAA30852.1; PID:g163978
C,Genetics:
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interferon-alpha - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
A;Itler: A: Hauptmann, R.; Adolf, G.R.; Swetly, P.
A;Title: Structure and expression in Escherichia coli of canine interferon-alpha genes.
A;Reference number: 146204; MUID:87281775; PMID:3039013
A;Accession: I46206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-187 <HIM>A;Residues: 1-187 <HIM>A;Residues: 1-187 <HIM>A;Residues: 1-187 <HIM>A;Residues: 1-187 <HIM>A;Residues: 1-180 <HI
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probable membrane protein YPO2952 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
                                                           Gaps
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         Best Local Similarity 80.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 1;
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Pred. No. 3.9e+02;
2; Mismatches 0,
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Pred. No. 3.9e+02;
2; Mismatches 0
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A;Molecule type: DNA
A;Residues: 1-187 <HI2>
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C,Superfamily: interferon alpha
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nes 3; Conserv
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16 CHSLC 20
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16 CHSLC 20
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38057
R;Skelton: J; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Bubmitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Accession: T38057
A;Accession: T38057
A;Readus: preliminary; translated from GB/EMBL/DDBJ
A;Readuse: L10 < SKE>
A;Readuse: 1-110 < SKE>
A;Readuse: 1-110 < SKE>
A;Residuse: 1-110 < SKE>
A;Residuse: 1-110 < SKE>
A;Residuse: 1-110 < SKE>
A;Experimental source: strain 972h-; cosmid c1E11
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Kseidues: 1-157 <MIL.>
A;Cross-references: UNIPROT:Q93904; EMBL:279603; PIDN:CAB01895.1; GSFDB:GN00028; CESP:M1
A;Experimental source: clone M163
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C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Schorella virus PBCV-1
C;Species: T105B #8equence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T175E
R;Graves, M.V.; Van Etten, J.L.
A;Graves, M.V.; Van Etten, J.L.
A;Reference number: Z18806
A;Reference number: Z18806
A;Reference number: T1785
A;Reference number: T1785
A;Reference number: T1785
A;Reference number: T1785
A;Residues: 1-131 AGRA-
A;Residues: 1-131 AGRA-
A;Residues: 1-131 AGRA-
A;Residues: 1-131 AGRA-
A;Residues: UNIPROT:Q89390; EMBL:U42580; NID:g4028896; PIDN:AAC96423.1
A;Genetics: A;Geneti
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Pred. No. 3e+02;
0; Mismatches
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A;Introns: 64/3; 78/3; 99/3; 109/1; 136/1
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Best Local Similarity 80.0%;
Matches 4; Conservative (
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A;Introns: 33/3; 43/2; 54/3; 58/2
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A;Gene: SPDB:SPAC1E11.02
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Matches 4; Conserv
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A;Gene: CESP:M163.6
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C;Complex: part of an enzyme complex containing a heterotrimer (flavoprotein, iron-sulfe C;Function:
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; V.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Ronney, T.; Rowley, D.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwarz, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUD:21016719; PMID:11130712
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C; Species: Yersinia pestis
C; Date: O.S.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession: AG0041
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R; Parkhill, J.; Wren, C.; Prentice, M.B. R; Parkhill, J.; Wren, C.; Pougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                       A,Cross-references: EMBL:X51509, NID:g48511; PIDN:CAA35876.1; PID:g48514
C;Genetics:
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Pred. No. 4.68+02;
0; Mismatches 1; Indels
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Pred. No. 4.9e+02;
2; Mismatches 0; Indels
                     A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-239 <KOE>
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Matches 3; Conservative
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A; Residues: 1-260 <STO>
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A; Accession: S10166
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N;Alternate names: fumarate reductase chain B
C;Species: Wolinella succinogenes
C;Date: 03-Jun-1993 #sequence_revision 19-Jul-1996 #text_change 12-Jul-2004
C;Accession: C44954; S10166
C;Accession: C44954; S10166
R;Lauterbach, F; Koerriner, C.; Albracht, S.P.J.; Unden, G.; Kroeger, A.
Arch. Microbiol. 154, 386-393, 1990
A;Title: The fumarate reductase operon of Wolinella succinogenes. Sequence and expression
A;Recreace number: A44954; MUID:91058386; PMID:2244791
A;Accession: C44954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 cLAU>
A;Residues: 1-239 cLAU>
A;Residues: 1-239 cLAU>
A;Residues: 1-239 cLAU>
A;Cos8-references: UNIPROT:P17596; GB:X51509; NID:948511; PIDN:CAA35876.1; PID:948514
A;Residues: 1-239 cLAU>
A;Cos8-references: UNIPROT:P17596; GB:X51509; NID:348511; PIDN:CAA35876.1; PID:948514
A;Reference number: S10164; MUID:90355847; PMID:2388563
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0359
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Accession: AC0359
A;Accession: AC0359
A;Accession: AC0359
A;Molecule type: DNA
A;Residues: 1-227 cKUR>
A;Residues: 1-227 cKUR>
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A;Gene: YP02952
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Nypotherical protein DKFZp434B217.1 - human (fragment)

C,Species: Homo sapiens (man)

C,Species: 13-Jan-2000 #text_change 09-Jul-2004

C,Accession: T43487

R,Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, December 1999

A,Reference number: Z22514

A,Reference number: Z22514

A,Status: preliminary

A,Status: preliminary

A,Status: preliminary

A,Status: UNIRROT:09UF79; EMBL:AL133566

A,Experimental source: adult testis; clone DKFZp434B217

C,Genetics:
A,Rote: DKFZp434B217.1

C,Superfamily: kexin; subtilisin homology
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80.0%; Pred. No. 4.5e+02;
iive 0; Mismatches 1;
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60.0%; Pred. No. 4.5e+02;
ive 1; Mismatches 1;
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Best Local Similarity 60.0
Matches 3; Conservative
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Matches 4; Conserv
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A;Molecule type: mRNA
A;Rosidues: 1-351 <TOD>
A;Cross-references: UNIPROT: Q9R0Q2; DDBJ: AB025230; NID: g5921091; PIDN: BAA84578.1; PID: g55
C;Genetics:
A;Gene: bIt
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Repwords: disulfide bond; glycoprotein; receptor; signal transduction; transmembrane pa
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R; Kanter, H.L.; Saffitz, J.E.; Beyer, E.C.
J. Mol. Cell. Cardiol. 26, 861-868, 1994
A; Title: Molecular cloning of two human cardiac gap junction proteins, connexin40 and cor A; Title: Molecular cloning of two human cardiac gap junction proteins, connexin40 and cor A; Title: Molecular cloning of two human cardiac gap junction proteins, connexin40 and cor A; Reference number: 138429
A; Reference number: 138429
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Mesidues: 1-358 cRES>
A; Cross-references: EMBL: U03486; NID: 9416327; PIDN: AAA60457.1; PID: 9416328
C; Superfamily: gap junction protein
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Cispeciaes: Percomyerous maniculatus (deer mouse)
Cispeciaes: Percomyerous maniculatus (deer mouse)
Cispeciaes: Percomyerous maniculatus (deer mouse)
Cispeciaes: Paral-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
Cistecession: A49107
Rizheng, Y.W.; Bey, M.; Liu, H.; Pelder, M.R.
J. Biol. Chem. 268, 249313-24939, 1993
A;Title: Molecular basis of the alcohol dehydrogenase-negative deer mouse. Evidence for charactering number: A49107; MUID:94043358; PMID:8227055
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A;Molecule type: mRNA
A;Residues: 1.375 - CZHE>
A;Cross-references: UNIPROT:P41680; GB:L15703; NID:g416387; PIDN:AAA40591.1; PID:g416388
C;Comment: The class I alcohol dehydrogenases are pyrazole-sensitive and have a high acti
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                                                                                                 Cippedies: Rattus norvegicus (Norway rat)
Cipate: 03-Dec-1999 #text_change 09-Jul-2004
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cipate: 07-199 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cipate: 07-199 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cipate: 07-199 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
RiToda, A.; Yokomizo, T.; Masuda, K.; Nakao, A.; Izumi, T.; Shimizu, T.
Biochem. Biophys. Res. Commun. 262, 806-812, 1999
A; Title: Cloning and characterization of rat leukotriene B4 receptor.
A; Reference number: JC7096; MUID:99400454; PMID:10471406
A; Molecular Dipate Dipate
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
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Pred. No. 6.2e+02;
0; Mismatches 1; Indels
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82.4%; Score 28; DB 2; Length 351;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
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A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUD:21470413; PMID:11586360

A; Accession: AG0041

A; A; Accession: AG0041

A; Residue: preliminary

A; Molecule type: DNA.

A; Residues: 1-290 «KUR»

A; Crose-references: UNIPROT: Q8ZIZ9; GB: ALS90842; PIDN: CAC89194.1; PID: g1S978433; GSPDB: C; Genetics:

A; Gene: rhaR

C; Superfamily: hypothetical protein b2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    friziled protein-2 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Jobate: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004 C;Accession: JE0174 E;Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D. Biochem. Biophys. Res. Commun. 247, 287-293, 1998 A;Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas. A;Reference number: JE0174; MUID:98308108; PMID:9642118
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A;Experimental source: clone F49A5
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T22393
R;Mortimore, B.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19560
A;Reference number: Z19560
A;Accession: T22393
A;Reference number: Library, November 1996
A;Reference number: Langlated from GB/EMBL/DDBJ
A;Reference number: Langlated from GB/EMBL/DDBJ
A;Reference number: DNA
A;Residues: 1-308 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 290;
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80.0%; Pred. No. 5.6e+02;
cive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    82.4%; Score 28; DB 2; I
80.0%; Pred. No. 5.3e+02;
:ive 0; Mismatches 1;
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A;Residues: 1-295 <HUN>
A;Cross-references: UNIPROT:Q9HAP5
C;Genetics:
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Best Local Similarity 80.0°
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Matches 4, Conservative
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Matches 3; Conservative
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114 CHSLC 118
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A,Map position: 5
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82.4%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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A; Residues: 1-424 <DEK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <YAO>
                                                                               CHEVC 54
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A, Status: preliminary
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A;Gene: Adh-1
C;Complex: homodimer (A2 isozyme)
C;Complex: homodimer (A2 isozyme)
C;Complex: homodimer (A2 isozyme)
C;Complex: homodimer set the oxidation of primary and secondary alcohols to aldehydes an A;Pathway: alcohol degradation
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Reywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor F;2-375/Product: alcohol dehydrogenase alpha #status predicted «MAT>
F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;35-34/Region: beta-alpha-beta NAD nucleotide-binding fold
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F;47,68.175/Binding site: zinc, actalytic (Cys) #status predicted
F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P16320; EMBL:X15469; NID:97962; PIDN:CAA33497.1; PID:97964
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 844909
A;Bescription: Sequence of the C. elegans cosmid ZK686.
A;Accession: S44909
A;Accession: S44909
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-407 < DNA
A;Residues: 1-407 < DNA
A;Coss-references: UNIPROT:P34670; EMBL:L17337; NID:g304345; PID:g304346
C;Genetics:
A;Introns: 156/3; 190/1; 212/3; 333/1
C;Keywords: DNA binding; nucleus
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Pred. No. 6.7e+02;
1; Mismatches 1; Indels
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82.4%; Score 28; DB 2; Length 407;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        82.4%; Score 28; DB 1; Length 375;
80.0%; Pred. No. 6.4e+02;
ive 0; Mismatches 1; Indels
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A; Residues: 1-403 <TEM>
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Best Local (
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Gaps

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C;Superfamily: thyroid hormone receptor; erbA transforming protein homology C;Keywords: DNA binding; nucleus; thyroid hormone receptor; transcription regulation; zi E;59-335/Domain: erbA transforming protein homology <BRBA> F;61-81/Region: zinc finger F;99-123/Region: zinc finger
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A55089; S51011
R;Sugimoto, T.; Saito, M.; Mochizuki, S.; Watanabe, Y.; Hashimoto, S.; Kawashima, H. R;Sugimoto, T.; Chm. 259; 270882-7092, 1994
A;Title: Molecular cloning and functional expression of a cDNA encoding the human V-1b v
A;Reference number: A55089; MUID:95014580; PMID:7929452
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A; Residues: 1-424 < SUG>
A; Cross-references: UNIPROT: P47901; GB: D31833; NID: 9563981; PIDN: BAA06621.1; PID: 9563982
A; Cross-references: UNIPROT: P47901; GB: D31833; NID: 9563981; PIDN: BAA06621.1; PID: 9563982
A; Cross-references: UNIPROT: P47901; GB: D31833; NID: 9563981; PIDN: BAA06621.1; PID: 9563982
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A;Note: the sequence from Fig. 2A is inconsistent with that from Fig. 1 in having 371-11
C;Superfamily: oxytocin receptor
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:P18115; GB:M35344; NID:9214831; PIDN:AAA49970.1; PID:9214832
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FBBS Lett. 356, 215-220, 1994
A;Title: Cloning and characterization of the human V3 pituitary vasopressin receptor.
A;Reference number: S51011; MUID:95104418; PMID:7805841
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thyroid hormone receptor alpha-B - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 09-Jul-2004
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                                                                                                                                                 RiYacita, Y.; Shi, Y.; Brown, D.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7090-7094, 1990
Affille: Kanopue laevie alpha and beta thyroid hormone receptors. A;Reference number: A36067; MUID:90384953; PMID:2402492
A;Accession: B36067
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Pred. No. 6.9e+02;
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60.0%; Pred. No. 7e+02;
ive 1; Mismatches
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completed: July 27, 2005, 00:01:48
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A; Gene: bloA
A; Start codon: GTG
C; Superfamily: beta-alanine-pyruvate transaminase
C; Superfamily: beta-alanine-pyruvate (c; Superfamily: 
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S58882
Sprotein kinase Cds1 (EC 2.7.1.-) [validated] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S58882; S71846; \( \frac{74}{41204}; \) \( \frac{75}{452473} \)
C;Accession: S58882; S71846; \( \frac{74}{41204}; \) \( \frac{752473}{41204} \)
Nature 374, M-199, 1995
A;Title: A Kinase from fission yeast responsible for blocking mitosis in S phase.
A;Reference number: S58882; MUID:95240713; PMID:7723827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:036407; EMBL:AF005370; NID:g2337967; PIDN:AAC58104.1; PID:g2 C,Genetics:
A;Introns: 17/1
C;Superfamily: saimiri herpesvirus 52K immediate-early protein
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                                                                   Cispecies: alcelaphine herpesvirus 1
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Cispecies: alcelaphine herpesvirus 1
Cispecies: A. Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
Cispecession: T03152
Rishsser, A.; Filanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: Z14440, MUID:97404659; PMID:9261371
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1; Mismatches 1; Indels
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A; Residues: 1-436 <ENS>
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A;Residues: 1-455 <GLO>
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A;Status; Dreliminary; nucleic acid sequence not shown
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A;Rostdens 1.460 *RURA.
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A;Rostdens 1.1404 *RURA.
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Q74nl5 nanoarchaeu Q6aav7 propionibac Q81bp3 plasmodium Q8y2b0 ralaconia s Q993m6 dictyosteli Q993m6 auconomous P34717 bovine rote P27586 porcine rot Q9py95 human rotav Q9m1q8 arabidopsis	071159 kilham rat P36311 parvovirus P07300 murine minu P03133 hamerer par P88899 kilham rat Q8914 rat minute Q8918 rat minute Q8918 rat minute Q8918 mouse parvo Q84363 murine minu Q84363 murine minu Q84363 murine minu Q66822 oryza sativ Q67xdu9 oryza sativ Q67xdu9 oryza sativ	Q84488 vibrio vuln Q7mfrz vibrio vuln Q803t4 mus musculu Q803t3 rana tigrin Q8twx8 methanopyru Q910i9 human cytom Q6sx8 human cytom Q914p8 human cytom Q914p9 human cytom Q914p7 human cytom Q914p7 human cytom Q69029 human cytom Q69029 human cytom Q69029 human cytom Q69029 human cytom	human human mus mw mus mw mus mw ectocs ectocs ectocs homo homo homo homo homo brachy
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The FANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
whaleysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN=C57BIJ/6J; TISSUE=Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Pukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imochani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konon H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS'BL/60; TISSUB=Testis; MEDLINE=99279253; PubMed=10349616; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                           01-MAR-2004 (TrEMBLrel. 17, Last sequence update)
M1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
M1s musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700127D06 product:similar to tissue kallikrein (EC
3.4.21.35), submandibular mGK-2.
Name=1700127D06Rik;
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibate K., Itoh M., Alzawa K., Magaoka S., Sasaki N., Carninci P., Sumi N., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., RTKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000)
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CS7BL/66; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORtium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                  114 AA.
                                                                                  PRT;
                                                                                  PRELIMINARY;
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                                                                                                         090974;
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STRAIN=TB40B, and 16yuek;
MEDLINE=21635521; PubMed=1177341B;
Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
"Identification of glycoprotein gpTRL10 as a structural component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K
Muramatsu M., Hayashizaki Y.;
Submitred (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO07298; BAB24941.1; -.
                                                                                                                                                        MGD; MGT:197429; 1700127D06Rik.
MGD; MGT:197429; 1700127D06Rik.
GO; GO:0008233; F:Erpeptidase activity; IEA.
GO; GO:0004295; F:Erpeptidase activity; IEA.
GO; GO:000609; F:Erpeptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001099; Trypsin; I.
SMART; SM00029; Trypsin; I.
SMART; SM00029; Trypsin; I.
PROSITE; PS50240; TRYPSIN DOM; I.
PROSITE; PS00135; TRYPSIN DOM; I.
PROSITE; PS00135; TRYPSIN SER; I.
Hydrolase; Percease; Serine protease.
SEQUENCE 114 AA; 13082 MW; CF6C05A967C47546 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human cytomegalovirus.";
J. Virol. 76:1450-1460[2002).
BEMBL; AF432092; AAL27446.1; -.
EMBL; AF432084; Cytomega TRL10; 1.
Pfam: PP06684; Cytomega TRL10; 1.
SEQUENCE 170 AA; 18940 MW; B496EE560IE33739 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF6C05A967C47546 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 70;
ive 0; Mismatches
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SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Goldmanth A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Garninci P., Chen H., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sarou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                              The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 34; DB 2; Length 238; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 34; DB 2; Length 235. 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                      Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AE017119; AAPS5005.1; -. Gramene; Q7XC69; -.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein At2g45010 (Fragment).
01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein. ORFNames-OSJNBa0042H09.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pfam; PF04749; DUF614; 1.
IIGRFAMS; TIGR01571; A_thal_CyB_rich; 1.
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InterPro; IPR006461; DUF A_thal_Cys.
Pfam; PF04749; DUF614; 1.
TIGRRAMS; TIGR01571; A_thal_Cys_rich; 1.
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                                                                                                                                                      Shrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                 Science 300:1566-1569,(2003)
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                       NCBI_TaxID=39947;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                         PubMed=15105547; DOI=10.1099/vir.0.79888-0;
Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L. Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C., Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AC079874; AAL79784.1; -.
                                                                                                                                                                         Davison A.J.;
"Genetic content of wild-type human cytomegalovirus.";
J. Gen. Virol. 85:1301-1312(2004).
EMBL; AY446863; AAR31286.1; -...
InterPro; IPR009284; Cytomega TRL10.
Pfam; PF06084; Cytomega TRL10; 1.
SEQUENCE 170 AA; 18942 MW; 8C851AB8E3473D71 CRC64;
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SEQUENCE 235 AA; 25948 MW; 11D13F750B1046F7 CRC64;
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1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein OSJNBa0042H09.16.
Name=OSJNBa0042H09.16;
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 2;
100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0
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InterPro; IPRO06461; DUF_A_thal_Cys.
Pfam; PF04749; DUF614; 1.
TIGRFAMS; TIGR01571; A_thal_Cys_rich; 1.
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Q7XC69;
01-OCT-2003 (TrEMBLrel. 25, Created)
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hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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hes 5; Conserv
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                                                    SEQUENCE FROM N.A.
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             NCBI_TaxID=10359;
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OBSBA1; QBSBA1

RESULT 4 Q8SBA1

Best Loca Matches

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Gaps

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Matches

8 a RESULT 5 Q7XC69 ID Q7XC0 AC Q7XC0 DT 01-00

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P349 (Fragment).
Citrus tristeza virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
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Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
Iturriaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hauan V.W., Lee J.M.,
Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
Yu G., Yuan S., Chen H., Cheuk K., Jones T., Kim C.J., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
Bcker J.R., Theologis A.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX120735, AAM53291.1; -.
EMBL, AX007559, AAM53291.1; -.
EMBL, AX18360; BAC42974.1; -.
EMBL, BT000360; AAN156791.; -.
EMBL, BT000360; AAN156791.; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martinez-Soriano J.P.; "Molecular analysis of Citrus tristeza virus isolates from Mexico."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AY652915; AAT75285.1; -.
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; IndelB
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293 AA; 32161 MW; 170A2DC266A948AF CRC64;
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Q692Q5;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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InterPro; IPRO06461; DUF_A_thal_Cys.
Pfam; PF04749; DUF614; 1.
TIGRFAM8; TIGR01571; A_thal_Cys_rich; 1.
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5; Conservative
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1es 5; Conservative
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Q692Q5
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069206
1D 06920
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DT 25-00
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MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.,
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Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
Palm C.J., Boweer L., Jones T., Banh J., Carninci P., Chen H.,
Palm C.J., Bowser L., Jones T., Bah, P., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Sacou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hasshizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyte, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Haas B.J., Volfovsky N., Town C.B., White O., Salzberg S.L., "Feldmann K.A., Flavell R.B., White O., Salzberg S.L., "Feldman K.A., Flavell R.B., White O., Salzberg S.E.,"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein At2945010.
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Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                              244 AA
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                                                                                                                                                           PRELIMINARY;
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106 CHAVC 110
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Citrus tristeza virus.
                                                                                                                                                                                                                                                                                                        118 CHAVC 122
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NCBI_TaxID=12162;
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Q692Q9
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Viruses; seRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
VCBI_TaxID=12162;
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Closterovirus.
NCBI_TaxID=12162;
                                                            Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V., Iturriaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R., Martinez-Soriano J.P.; "Molecular analysis of Cirus tristeza virus isolates from Mexico."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,

Iturriaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,

Martinez-Soriano J.P.,

"Molecular analysis of citrus tristeza virus isolates from Mexico.";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AY652913; AAT75283.1; -.
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                                                                                                                                                                                                                                                         293 293 293 293 AW; 82B2464AC4EE6348 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P349 (Fragment)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P349 (Fragment).
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Best Local Similarity 100.
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                                              SEQUENCE FROM N.A.
NCBI_TaxID=12162;
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AC 069207
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P349 (Fragment).
Citrus tristeza virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
NCBI_TaxID=12162;
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Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
Iturriaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
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Iturriaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
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EMBL; AY652910; AAT75280.1; -.
NON_TER 1 1 1.
NON_TER 293 A93
SEQÜENCE 293 AA; 32074 MW; D21D1D6D2A3D7ECC CRC64;
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"Molecular mailysis of Citrus tristeza virus isolates from Mexico.";
"Molecular mailysis of Citrus tristeza virus isolates from Mexico.";
"Molecular mailysis of Citrus tristeza virus isolates.
EMBL; AX652911; AAT75281.1; -.
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NON TER 293 AA; 32746 MW; CE5845D4DFCB7775 CRC64;
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Q692Q9 PRELIMINARY; PRT; 293 AA. Q692Q9; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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100.0%; Score 34; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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Viruses; șsRNA positive-strand viruses, no DNA stage; Closteroviridae;
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Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
Iturriaga Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
Iturriaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
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                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinez-Soriano J.P.;
"Molecular analysis of Citrus tristeza virus isolates from Mexico.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX652909; AAT75279.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martinez-Soriano J.P.; "Molecular analysis of Citrus tristeza virus isolates from Mexico."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AX652908; AAT75278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                           Indels
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Last annotation update)
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100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                     Created)
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                          118 CHAVC 122
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AC 0692R
AC 0692R
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0692R1
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101-101-1020 (TERBELAINARY)

101-101-2020 (TERBELAEL 21, Lest esquence update)

101-101-2020 (TERBELAEL 21, Lest esquence update)

102-007-2020 (TERBELAEL 22, Lest annotation update)

102-007-2020 (TERBELAEL 22, Lest annotation update)

103-007-2020 (TERBELAEL 22, Lest annotation update)

104-007-2020 (TERBELAEL 22, Lest annotation update)

105-007-2020 (TERBELAEL 22, Lest annotation update)

105-007-2020 (TERBELAEL 22, Lest annotation update)

106-007-203 (TERBELAEL 22, Lest annotation update)

107-007-2020 (TERBELAEL 22, Lest annotation update)

108-007-203 (TERBELAEL 22, Lest annotation update)

108-007-203 (TERBELAEL 22, Lest annotation update)

109-007-203 (TERBELAEL 22, TERBELAEL 22, Lest annotation update)

109-007-203 (TERBELAEL 22, TERBELAEL 22, Lest annotation update)

109-007-203 (TERBELAEL 22, TERBELAEL 22, TERBELAEL 22, TERBELAEL 23, TER
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PRELIMINARY;
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SEQUENCE FROM N.A.
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PubMed=12447439; DOI=10.1038/nature01183;
Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao O., Ying K., Yu S., Tang Y.,
Heng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang X.,
Cai Z., Ren S., Lv G., Gu W., Zha G., Tu Y., Hu Q., Zhang X.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
                                                                                                                                                                                        MEDLINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Calniker S.E.; "Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective."; Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Capchnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a
Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.W.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 381 AA, 43725 MW; 012595FB8830BC9C CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL; AE003685; AAF54486.2; --
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Name=OSJNBb0026E15.3;
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01-OCT-2003
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Q7X8U8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Psychrobacter sp. Ant300.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
NCBI_TaxID=235460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipase.
Name-lip;
Psychrobacter sp. (strain Stl).
Bsychrobacters sp. (strain Stl).
Bacteria; Proteobacteria, Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 34; DB 2; Length 382; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Han B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 34; DB 2; Length 400; 100.0%; Pred. No. 2.2e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               3OX; 1.
42864 MW; CF7B92144C7C8E2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9L514;
1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
                                                                   "Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AA
                                                                                                                                                InterPro; IPR001810; P-box.
InterPro; IPR001810; P-box.
InterPro; IPR0101810; Gl_oxid_central.
InterPro; PF004 F. Pbox; 1.
SMART; SM00256; PBOX; 1.
TIGRPAMS; TIGR01640; P.box_a880c_1; 1.
PROSTIE; PROST181; FBOX; 1.
SEQUENCE 382 AA; 42864 MW; CF7B921440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                            Nature 420:316-320 (2002).
EMBL; AL607008; CAE03685.2; -.
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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Query Match
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                       TRAINSEL!

A Kulakova L., Galkin A., Kurihara T., Yoshimura T., Esaki N.;

L Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

R Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AFZ6007; AAF70342.1;

R GJ, GG.001677; F. Hydrolase activity; IEA.

R GJ, GG.0008152; P. metabolism; IEA.

R GJ, GG.0008152; P. metabolism; IEA.

R InterPro; IPR006025; Pept M Zn BS.

R InterPro; IPR000379; Ser_estrs.

R ROSITE; PS01173; LIPASE GDXG HIS; 1.

PROSITE; PS01173; LIPASE GDXG HIS; 1.

PROSITE; PS01142; ZINC_PROTEASE; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 34; DB 2; Length 400; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; Q9FRE7; -.
InterPro; IRR001810; F-box.
Pfam; PP00646; F-box; 1.
SMART; SM00756; FBOX; 1.
Hypothetical protein.
SEQUENCE 424 AA; 46722 MW; 19B44CE09CF41F02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OSJNBa0013M12.13.
Name-OSJNBa0013M12.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 AA.
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Moraxellaceae; Psychrobacter.
NCBI_TaxID=125076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AC082644; AAG46124.1;
                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity luv...
5; Conservative
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                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CHAVC 5
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09FRE
AC 09FRE
AC 09FRE
DT 01-MAD
DT
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Q7QVC3
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STRAIN=domestic breed; TISSUE=Aorta;
STRAIN=domestic breed; TISSUE=Aorta;
Stocker C., Sugars K., Yarwood H., Delikouras A., Dorling A.,
Stocker C., Sugars K., Yarwood H., Delikouras A., Dorling A.,
Lechler R., Landis C., Morley B., Haskard D.;
Tar indothelial cells by cytokines.",
T. Immunol. 0:0-0(1999).
The strain of portion of transparent in the strain and characterization of TrS induction on the strain and characterization of TrS induction on the strain and train and the strain and the strain
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Subs scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olsen G.J., Sogin M.L.; included lamblia genome."; Draft sequence of the Giardia lamblia genome."; submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                               GLP 542 47587 46190.
Giardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
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EMBL, AACBO1000083; EAA39016.1; ---
GO; GO:00055489; F:electron transporter activity; IEA.
GO; GO:000518; P:electron transport; IEA.
CO; GO:000518; P:electron transport; IEA.
InterPro; IPR00450; F:electron transport; IEA.
InterPro; IPR00450; Grow Fac_recept.
INTERPRO; PR0053; AFE4SREDOXIN.
PRINTS; PR0053; AFE4SREDOXIN; UNKNOWN 1.
SEQUENCE 465 AA; 48977 MW; 83D00ABAS357D7DC CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Intercellular adhesion molecule-1 precursor.
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0;
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Matches 5; Conservative
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537
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Citrus tristeza virus
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                                                                                                                                                         Gaps
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Oryza sativa (jakonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=WB C6;
MOTAISON H.G., MCARTHUR A.G., Adam R.D., Aley S.B., Gillin F.D.,
Olsen G.J., Sogin M.L.;
"Draft sequence of the Glardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                   100.0%; Score 34; DB 2; Length 537; 100.0%; Pred. No. 2.9e+02; Attive 0; Mismatches 0; Indels
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GLP 572 62459 60477.
Glardia lamblia ATCC 50803.
Bukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
   537 AA; 58430 MW; 47DA0F0F3C75CD54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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Best Local Similarity 100..
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96 CHAVC 100
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070247
AC 070244
AC 07024
DT 01-MA
DT 01-MA
DT 01-MA
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OS GLAID
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069784
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CC -1- CAUTION: The sequence shown here is derived from an profile and the sequence shown here is derived from an proliferance date whose genome shocking (GG) 600:00506; Pitch is the sequence activity; IEA.

BROWL, ACCONDONOS; Palanch transport; IEA.

BROWL, COCONDOSCOS; Pitch in binding; IEA.

BROWL, COCONDOSCOS; Pitch in binding; IEA.

BROWL, COCONDOSCOS; Pitch in binding; IEA.

BROWLED REPORT (GG) 200:00506; Pitch in binding; IEA.

BROWLED REPORT (GG) 200:00506; Pitch in binding; IEA.

BROWLED REAL (G
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01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 100...
5; Conservative
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Matches 5; Conservative
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Citrus tristeza virus
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NCBI_TaxID=12162;
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Q9WID7
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STADULENCE FROM: N.T.

MEDLINE=20007030; PubMed=10541017; DOI=10.1023/A:1008127224147;

A Yang Z.N. Mathews D.M., Dodds J.A., Mirkov T.E.;

"Molecular characterization of an isolate of citrus tristeza virus that causes severe symptoms in sweet orange.";

"Molecular characterization of an isolate of citrus tristeza virus that causes severe symptoms in sweet orange.";

"Molecular characterization of an isolate of citrus tristeza virus that causes severe symptoms in sweet orange.";

"Molecular characterization and tristering that causes severe symptoms in sweet orange.";

"Molecular characterized passons.";

"Mol
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3115 AA; 347072 MW; B406EA0FB38E73F9 CRC64;
                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last sequence update)
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PRT; 3115 AA
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PRELIMINARY;
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                                                                                                                                                                                                            347-kDa polyprotein.
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SEQUENCE 3
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091FX
001FX
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WEDLINE=99190444; PubMed=10092023;

WEDLINE=99190444; PubMed=10092023;

WEDLINE=99190444; PubMed=10092023;

A Vives M.C., Rubio L., Lopez C., Navas-Castillo J., Albiach-Marti M.R.,

BA Vives M.C., Valori J., Flores R., Moreno P.;

The complete genome sequence of the major component of a mild citrus

RT tristeza virus isolate.";

J. Gen. Virol. 80:811-816(1999).

REMEL, Y18420; CAA77161.1;

DR GO, GO:0008174; F:RNA helicase activity; IEA.

GO, GO:0008174; F:RNA helicase activity; IEA.

DR GO, GO:0003724; F:RNA helicase activity; IEA.

GO, GO:0003784; F:RNA helicase activity; IEA.

DR GO, GO:0003969; P:RNA processing; IEA.

GO, GO:0003969; P:RNA processing; IEA.

DR GO, GO:000596; P:RNA processing; IEA.

DR GO, GO:0019079; P:Viral genome replication; IEA.

InterPro: IPR00056; Viral helicasel.

BR InterPro: IPR00588; V.methyltrans.

DR Ffam; PF01443; Viral helicasel;

DR Ffam; PF01443; Viral helicasel;

SEQUENCE 3115 AA; 346982 MW; 3EEA612F605D5045 CRC64;
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Citrus tristeza virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Closterovirus.
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100.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 0; Indels
InterPro; IPR008749; Peptidase C42.
InterPro; IPR00266; Viral helicasel.
InterPro; IPR002589; V methylrrans.
Pfam; PF05533; Peptidase C42; 2.
Pfam; PF01443; Viral helicasel; 1.
Pfam; PF0160; Vmethyltransf; 1.
SEQUENCE 3115 Aa; 346874 MW; 6897F494ED25AD63 CRC64;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 1.5e+03;
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1 CHAVC 5
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Polyprotein.
SEQUENCE 3
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05-JUL-2004
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ID Q9N9M2
AC Q9N9M2;
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Q74N15;
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                     MEDLINE=99907427; PubMed=10377432; DOI=10.1073/pnas.96.13.7433; Satyanarayana T., Gowda S., Boyko V.P., Albiach-Marti M.R., Mawassi M., Navas-Castillo J., Karasev A.V., Dolja V., Hilf M.E., Lewandowski D.J., Moreno P., Bar-Joseph M., Garnsey S.M., Dawson W.O.; terminal sequences for replication."; Proc. Natl. Acad. Sci. U.S.A. 96:7433-7438(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                       MEDLINE=22836522; PubMed=12954215; DOI=10.1016/S0042-6822(03)00387-8; Satyanarayana T., Gowda S., Ayllon M.A., Dawson W.O.; "Frameshift mutations in infectious cDNA clones of Citrus tristeza virus: a strategy to minimize the toxicity of viral sequences to Escherichia coli.";
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SEQUENCE FROM N.A.

STRAIN=seedling yellows strain;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

Lubinitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB046398; BAB18522.1;

R GO; GO:00003724; F:RNA binding; IEA.

R GO; GO:0003724; F:RNA binding; IEA.

R GO; GO:0003726; F:RNA binding; IEA.

R GO; GO:0003726; F:RNA binding; IEA.

R GO; GO:0003726; F:RNA poincese activity; IEA.

R GO; GO:0003726; F:RNA poincese activity; IEA.

R GO; GO:0003726; F:RNA poinceseing; IEA.

R GO; GO:0003729; P:Viral genome replication; IEA.

R InterPro; IPR008749; Pepildase C42.

R InterPro; IPR008666; Viral helicasel.

R Pfam; PF0543; Viral helicasel; 1.

R Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                        ESULITION OF 131:481-491(2003).

REMBL; AY170468; AA012715.1; ...

REMBL; AY170468; AA012715.1; ...

ROG; GO:0003723; F:RNA binding; IEA.

ROG; GO:0003724; F:RNA binding; IEA.

ROG; GO:0003768; F:RNA helicase activity; IEA.

ROG; GO:000396; P:RNA-directed RNA polymerase activity; IEA.

ROG; GO:000396; P:RNA-directed RNA polymerase activity; IEA.

ROG; GO:000396; P:VIAI genome replication; IEA.

ROG; GO:0019079; P:VIAI genome replication; IEA.

RINEEPRO; IPRO06366; Viral helicase1.

InterPro; IPRO0568; V methyltrans.

R Pfam; PF0543; Peptidase (42.

R Pfam; PF05443; Viral helicase1; 1.

R Pfam; PF01660; Vmethyltransf; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             3122 AA; 348272 MW; D7084307FF0ED355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 34; DB 2; L
100.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Citrus tristeza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349-kDa polyprotein.
Name=p349;
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               SEQUENCE FROM N.A.
                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                  Polyprotein.
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q9DTG5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Possible RJS/HERC2-11ke protein (Possible herc2-related protein)
Name=LJ3665.04; Synonyms=P265.01;
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Submitted (DEC-2010) to the EMBL/GenBank/DDBJ databases.
EMBL, AL359775; CAB95249.2; -
EMBL, AL359716; CAD19412.1; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005612; P:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR000569; HECT.
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                                                Query Match
100.0%; Score 34; DB 2; Length 3132;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
WINDLINE=98146435; PubMed=9477341;
WHOME A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:115-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001400; Somatctropin.
InterPro; IPR003877; SPRY_receptor.
Pfam; PF00622; SPRY; 2.
SMART; SM00119; HECT; 1.
PROSITE; PS003138; SOMATCTROPIN 2; UNKNOWN 1.
SEQUENCE 5636 AA; 593224 MW; 84D6DDD4B0A5E694 CRC64;
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3132 AA; 349380 MW; 4A7A1DDD7DEC9463 CRC64;
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Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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(TrEMBLrel. 27, Last sequence update)
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es 5; Conserv
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97.1%;
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Best Local Similarity 80...
                                                               4; Conservative
                                                                                                                                                                                                                                                                      PRELIMINARY;
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                  Query Match
Best Local Similarity
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                                                                                                                                                       45 CHAIC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=36329;
                                                                                                            1 CHAVC 5
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                                                                                                                                                                                                                                                                                              Q8IBP3;
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QRIBP3
                                                             Matches
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STRAIN=KPAI11202 / DSM 16379;

STRAIN=KPAI11202 / DSM 16379;

Rubmed=15286373; DOI=10.1165/science.1100330;

Rubscapemann H., Henne A., Hoster F., Liesegang H., Wiezer A., Strittmatter A., Hujer S., Duerre P., Gottschalk G.;

The complete genome sequence of Propionibacterium acnes, a commensal of human skin.";

Cf human skin.";

Science 305:671-673(2004).

EMBL, AE01229; ATT82109.1; -.

ROG: GO:0016829; F12-C-methyl-D-erythritol 2,4-cyclodiphosphat. .; IEA.

GO: GO:0016829; F12-C-methyl-D-erythritol 2,4-cyclodiphosphat. .; IEA.

ROG: GO:0016829; F12-C-methyl-D-erythritol 2,4-cyclodiphosphat. .; IEA.

ROG: GO:0016829; F12-C-methyl-D-erythritol 2,4-cyclodiphosphat. .; IEA.

ROG: GO:0016829; F12-Spand biosynthesis; IEA.

RITHERPO: IPRO10225; MECDP_synth.

RITHERPO: IRRO0356; YgbB; 1.

RITHERPO: IRRO0356; YgbB; 1.

RITHERPO: IRRO0356; YgbB; 1.

RIGKFAMS; TICRO0161; ispF; 1.
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                                                                                                                                                                                                                    Waters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M., Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X., Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M., Soell D., Stetter K.O., Short J.M., Noorderwier M.;

"The genome of Nanoarchaeum equitans: insights into early archaeal rolution and derived parasitism.";

"The genome of Nanoarchaeum equitans: insights into early archaeal Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).

R EMBL; AE017199; AAR39222.1;

R GO; GO:0005499; F:electron transporter activity; IEA.

R GO; GO:0005506; F:iron ion binding; IEA.

R GO; GO:000518; P:electron transport; IEA.

R InterPro: IPR0001450; Fef45 ferredoxin.

R InterPro: IPR000345; Cytc_heme_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                    MEDLINE=22946215; PubMed=14566062; DOI=10.1073/pnas.1735403100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0353; 4FE4SFRDOXIN.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
FF6-46; Complete proteoms Iron: Iron-sulfur; Metal-binding.
SEQUENCE 75 AA; 7981 MW; B6656D8374ASCEF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-077-2004 (TrEMBLrel. 28, Created)
25-077-2004 (TrEMBLrel. 28, Last sequence update)
25-077-2004 (TrEMBLrel. 28, Last annotation update)
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 2; Length 75;
Pred. No. 72;
1; Mismatches 0; Indels
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168 AA; 16829 MW; DF6C56D1DD903042 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                  Archaea; Nanoarchaeota; Nanoarchaeum.
NCBI_TaxID=160232;
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Best Local Similarity 80.vv,
4; Conservative
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OrderedLocusNames=PPA0354;
                                            OrderedLocusNames=NEQ373;
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                                                                    Nanoarchaeum equitans
                                                                                                                                                            SEQUENCE FROM N.A.
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17 CHAIC 21
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Q6AAV7
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MEDLINE-21661879; PubMed=11823852; DOI=10.1038/415497a;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguiar P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502 (2002).
EMBL; AL646059; CAD13954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seger K., Murphy L., Harris D., Berriman M., Pain A., Hall N., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL844506; CAD50956.1; -.
HSSP; Q57679; 1B78.
GO; GO:0016797; F:hydrolase activity; IEA.
InterPro; IPR002637; Hamlp_like.
Pfam; PF01725; Hamlp_like; 1.
Hypothetical protein.
SEQUENCE 198 AA; 23080 MW; CE0AA63F011B3D3E CRC64;
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Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MAL7P1.110.
Name=MAL7P1.110;
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.1%; Score 33; DB 2; Length 198; 80.0%; Pred. No. 1.8e+02; ive 1; Mismatches 0; Indels
Score 33; DB 2; Length 168;
Pred. No. 1.5e+02;
                                                               0; Indels
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RSC0426.
                                                                                                                                                                                                                                                                                                                                                          198 AA
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                                                                  1; Mismatches
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280 CHAIC 284
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AC
TD VN34 ROTBS
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TD VN34 ROTBS
AC
DT 01-FEB-1994
DT 01-FEB-1994
DT 05-JUL-2004
DE Nonstructures
GN Name=S6;
OS Norners; des
CN Viruses; des
CN NCBL_TaxID=33
CN NC
                                                                                                                                                                                                                                                                                                                                        NON TER
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of Dictyostellum discoideum cathepsin D. Molecular cloning, gene disruption, endo-lysosomal localization and sugar modifications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Axz, and Ax-2;
MEDLINE=99454799; PubMed=10523518;
Journet A.M., Chapel A., Jehan S., Adessi C., Freeze H., Klein G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autonomous rat parvovirus RV-Y.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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97.1%; Score 33; DB 2; Length 273;
80.0%; Pred. No. 2.4e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               midutications. 1.

J. Cell Sci. 112:3833-3843(1999).

-- SIMILARITY: Belongs to peptidase family Al.

-- KASP; POO794; ACMS.

-- KASP; POO794; 4CMS.

-- CO GO:0004194; F: Cathepsin A activity; IEA.

-- GO: GO:0004194; F: Peptidase activity; IEA.

-- GO: GO:0006508; P: Peptidase activity; IEA.

-- GO: GO:0006508; P: Peptidase Al.

-- InterPro; IPR001461; Peptidase Al.

-- InterPro; IPR001969; Pept_Aspartic.

-- InterPro; IPR001969; Pept_Aspartic.

-- DETAIL CONTROL OF CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cathepsin D. CC8DE423AEA1A280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nonstructural protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Preprocathepsin D precursor (EC 3.4.23.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00141; ASP PROTEASE; 1.
Aspartyl protease; Hydrolase; Protease; Signal.
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                    383 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                          Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                            1 CHAVC 5
|||:|
94 CHAIC 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garin J.;
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     Query Match
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Q993M6
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076856
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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-!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=21102993; PubMed=11172095;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
Ball-Goodrich L.J., Johnson E., Jacoby R.;
Ball-Goodrich Minetics of two phenotypically different parvoviruses of rate.";
J. Gen. Virol. 82:537-546(2001).
BMBL, AR317913; AR274381.;
GO; GO:0019012; C:virion; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
InterPror; IPRO01257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; I.
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MEDILTE-3927578; PubMed-8389040;
Jánny B., Tsunemiteu H., Gentech J.R., Saif L.J., Glass R.I.;
"Nucleotide sequences of genes 6 and 10 of a bovine group C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                               97.1%; Score 33; DB 2; Length 397
80.0%; Pred. No. 3.48+02;
:ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indela
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                                                                                                                                                                                                                                                                                                                                                                          397 AA; 43959 MW; D62052E4767366BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Nonstructural RNA-binding protein 34 (NS34) (NCVP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 33; DB 1; L
80.0%; Pred. No. 3.4e+02;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine rotavirus (group C / strain Shintoku).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=33723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 AA
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InterPro; IPR001159; DS RBD.
InterPro; IPR001159; DS RBD.
Ffam; PF001035; dBrm; 1.
Pfam; PF01665; Rota_NSP3; 1.
SNART; SN00358; DSRM; 1.
RNOSITR; PS501137; DS_RBD; 1.
NONStructural protein; RNA-binding.
DOMAIN 384 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L12390; -; NOT ANNOTATED CDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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|||:|
103 CHAIC 107
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PRELIMINARY;
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153 CHAIC 157
                                                                                                                                                                                                                                                                                                                                                                         280 CHAIC 284
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09M108;
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071159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@alb.cib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y., Caul E.O., Clarke I.N.; uman group C rotavirus genes 6, 7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=91361567; PubMed=1653496;
Qian Y.A., Jiang B.M., Saif L.J., Kang S.Y., Ojeh C.K., Green K.Y.;
"Molecular analygis of the gene 6 from a porcine group C rotavirus
that encodes the NS34 equivalent of group A rotaviruses.";
Virology 184:752-757(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human rotavirus (group C / strain Bristol).
Viruses, dsRNA viruses, Reoviridae, Rotavirus, Human rotavirus C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%; Score 33; DB 1; Length 402;
80.0%; Pred. No. 3.4e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 AA; 45125 MW; 8B11F7AC7FB5135C CRC64;
                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Nonstructural RNA-binding protein 34 (NG34) (NCVP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                   Porcine rotavirus (group C / strain Cowden).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10916;
                                                                 402 AA
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InterPro; IPR001159; DS RBD.
InterPro; IPR001159; DS RBD.
Ffam; PF00035; dsrm; 1.
Pfam; PF01665; Rota NSP3; 1.
PROSITE; PS50137; DS RBD; 1.
Nonstructural protein; RNA-1niding.
DOMAIN 384 400 DRBM.
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J. Gen. Virol. 80:3181-3187(1999).
EMBL: AJ132203; CAB52751.1; -.
HSSP: P03536; 1KNZ.
GO; GO:0005622; C:intracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         James V.L.A., Lambden P.R., Deng Y., "Molecular characterisation of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol;
MEDLINE=20036633; PubMed=10567650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M69115; AAA47087.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 80.0 nes 4; Conservative
                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nonstructural protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 CHAIC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CHAVC 5
                  RESULT 39
VN34_ROTPC
ID VN34_ROTPC
AC P27586;
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Q9PY95
AC Q9PY95
DT Q1-MA
DT 01-MA
DT 
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein T17J13.120.
Name=T17J13.120;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NUBL TaxID=3702;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
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Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
97.1%; Score 33; DB 2; Length 428;
Best Local Similarity 80.0%; Pred, No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI38651; --
PIR; T48008; T48008.
GO; GO:0019012; C:virion; IEA.

GO; GO:0003125; F:double-stranded RNA binding; IEA.
InterPro; IPR001159; DS_RBD.
InterPro; IRR002893; Nota_NSP3.
Pfam; PF01065; Garm; 1.
Pfam; PF01665; Rota NSP3; 1.
SMART; SM00358; DSFW; 1.
PROSITE; PS0137; DS_RBD; 1.
NONSTRUCTURAL protein.
SEQUENCE 402 AA; 45327 MW; D2E3D7F14B6E2E23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003480; Transferase.
Pfam. PP02458; Transferase; 1.
Hypothetical protein.
SEQUENCE 428 AA; 47553 MW; 66C5155A161B26CA CRC64;
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071159;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-2004 (TrEMBLrel. 26, Last annotation update)
Nonstructural protein (Fragment).
                                                                                                                                                                                                                                                                                                             97.1%; Score 33; DB 2; I
80.0%; Pred. No. 3.4e+02;
ive 1; Mismatches 0;
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Best Local Similarity Bu.v.
Best Local 4; Conservative
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672 AA

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CONFLICT
SEQUENCE
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                                                                                                                          SO THE FEW NEW PRICE COURSE SERVING THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - FUNCTION: Seems necessary for viral DNA replication.
- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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                                                                                                                          "Rat parvovirus type 1: the prototype for a new rodent parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parvovirus Lulli.
Viruses, seDNA viruses; Parvoviridae, Parvovirinae; Parvovirus.
VCBI_TaxIb=35339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                             MEDLINE=98184569; PubMed=9525656;
Ball-Goodrich L.J., Leland S.E., Johnson B.A., Paturzo F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 33; DB 1; Length 668; 80.0%; Pred. No. 5.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%; Score 33; DB 2; Length 665; 80.0%; Pred. No. 5.4e+02; ive 1; Mismatches 0; Indels
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668 AA; 75846 MW; CAE69049F8F86B53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              665 AA; 75375 MW; 778E29043417E409 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1)
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Pfam; PF01057; Parvo NS1; 1.
ATP-binding; DNA replication; Noncapsid protein;
                                                                                                                                                                                                   EMBL; M81888; -; NOT_ANNOTATED_CDS.
PIR; A44276; A44276.
                                                                                                                                                                                                                                                                                                             InterPro; IPR001257; Parvo NS1
Pfam; PF01057; Parvo NS1; 1.
                                                                                                                                                           serogroup.";
J. Virol. 72:3289-3299(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pattern.";
Virology 192:339-345(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Nonstructural protein.
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Matches 4; Conserv
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ses 4; Conserv
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P36311;
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SEQUENCE
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AC VNCS PAVL3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- DOMAIN: The N-terminus (residues 1-275) possess a negative effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on transactivation (By similarity).
--- DOMAIN: The C-terminus (residues 543-672) possess an activation domain (By similarity).
--- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'DNA sequence comparison between two tissue-specific variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interacts with SYNCRIP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autonomous parvovirus, minute virus of mice.";
voldisk sadids Res. 13:3617-3633(1985).
-!- PUNCTION: Seems necessary for viral DNA replication.
-!- SUBUNIT: Forms homooligomers. Interacts with human SYNCRIP (By
                                                                                                                                                                                                                                                                                                                                      MEDLINE-86115415; PubMed-3502703;
Astell C.R., Gardiner B.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                              Murine minute virus (strain MVMi) (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Noncapald protein NS-1 (Nonstructural protein NS1) (NCVP1).
P07300; P10837;
01-APR-1988 (Rel. 07, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
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597 597 I -> L (in Ref. 2).
672 AA; 76140 MW, 25F025FE328B4DF0 CRC64;
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Pfam; PF01057; Parvo NS1; I.
ATP-binding; DNA replication; Noncapsid protein;
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80.0%; Pred. No. 5.5e+02;
tive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=85242059; PubMed=3855242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sahli R., McMaster G.K., Hirt B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M12032; AAA69567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prototype strain.";
J. Virol. 57:656-669(1986)
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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P03134;
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VNCS_MUMIV
ID VNCS.M
AC P03134,
DT 21-JUL-
DT 21-JUL-
DT 05-JUL-
DT 05-JUL-
DT NORGAP:
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             -i- FUNCTION: Seems necessary for viral DNA replication.
-i- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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Viruses, ssDNA viruses, Parvoviridae, Parvovirinae, Parvovirus.
NCBI_TaxID=172387;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
                                                                                                                                                                                                                                                                                                                                               97.1%; Score 33; DB 1; Length 672;
80.0%; Pred. No. 5.5e+02;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                  399 406 ATP (Potential).
672 AA; 75993 MW; 12F331142F72AAGD CRC64;
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Last annotation update)
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Last annotation update)
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InterPro; IPR001257; Parvo NS1.
Pfam; PF01057; Parvo NS1; T.
ATP-binding; DNA repTication; Noncapsid protein;
NOnsetructural protein.
NP BIND 399 406 ATP (Potential).
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80.0%; Pred. No. 5.5e+02;
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Best Local Similarity
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378 CHAIC 382
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P88899;
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Q8JV14;
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                                                                                                                                                                                                                MEDLINE=99102562; PubMed=9847309;
Harris C.E., Boden R.A., Astell C.R.;
Harris C.E., Boden R.A., Astell C.R.;
"A novel heterogeneous nuclear ribonucleoprotein-like protein
interacts with NSI of the minute virus of mice.";
J. Virol. 73:72-80(1999).
-I. FUNCTION: Seems necessary for viral DNA replication.
-I. SUBUNIT: Forms homooligomers. Interacts with human SYNCRIP.
-I. DOMAIN: The N-terminus (residues 1-275) possess a negative effect
                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
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MEDLINE=83112183; PubMed=6823009;
MEDLINE=81112183; PubMed=6823009;
MADGE S.L. III, Paradiso P.R.;
"Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybrid-arrested translation.";
                                                                                            MEDLINE-83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
          Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=10794;
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NCBI_TaxID=10799;
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21-JUL-1996 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
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76248 MW; 50298F27662E3C1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interacts with SYNCRIP.
                                                                                                                                                                                                   HOMOOLIGOMERIZATION, AND INTERACTION WITH SYNCRIP
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InterPro; IPR001257; Parvo_NS1.
Pfam; PF01157; Parvo_NS1; I.
ATP-binding; DNA replication; Noncapsid protein;
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80.0%; Pred. No. 5.5e+02;
tive 1; Mismatches 0;
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                                                                                                                                                                Nucleic Acids Res. 11:999-1018(1983).
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PIR; A03696; UYPVIM.
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Best Local Similarity 80...
4; Conservative
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DOMAIN 1 276
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672 AA;
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ID VNCS_PAVHH
AC P03133;
                                                                                                                                                  parvovirus
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Kilham rat virus.
Viruses; sebnA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=12441;
                                               Rat minute virus la.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=172385;
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80.0%; Pred. No. 5.Se+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;

Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;

Bubit ded (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF312882; AAM931275.1; -.

GO; GO:0019012; C:virion; IEA.

GO; GO:0019079; P:viral genome replication; IEA.

InterPro; IPR01257; Parvo NS1.

Fam; PF01057; Parvo NS1; Ī.

Nonstructural protein.

SEQUENCE 672 AA; 76059 MW; 63D8B9EBF99E07B3 CRC64;
                                                                                                                                            SEQUENCE FROM N.A.
MEDINE-22120170; PubMed=12124471;
MEDINE-22120170; PubMed=12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDINERS-22124471; MEDINERS-22120170; Wene C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.; wan C.H., Soderlund-Venermo of three newly recognized rat "Molecular characterization of three newly recognized rat
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nonstructural protein 1.
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nonstructural protein 1.
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J. Gen. Virol. 83:2075-2083(2002).
                                                                                                                                                                                                                        parvoviruses.";
J. Gen. Virol. 83:2075-2083(2002).
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Best Local Similarity 80.v.
A: Conservative
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08JV28;
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
VCBI_TaxID=172386;
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GO, GO: 0019012; C: virion; IEA.

GO, GO: 0019079; P: viral genome replication; IEA.

InterPro; IRR01257; Parvo NS1.

Fam. PF01057; Parvo NS1.

Nonstructural protein.

SEQUENCE 672 AA; 76201 MW; C2F1A71F6EF449A6 CRC64;
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80.0%; Pred. No. 5.5e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                           Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF332884; AAM93279.1; -
GO; GO:0019912; C:virion; IEA.
GO; GO:0019912; C:virion; IEA.
InterPro; IPR01157; Parvo NS1.
InterPro; IPR01157; Parvo NS1.
Nonstructural, protein.
SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;
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80.0%; Pred. No. 5.5e+02;
ive 1; Mismatches 0; Indels
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                                      MEDLINE-22120170; PubMed-12124471;
Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
"Molecular characterization of three newly recognized rat
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nonstructural protein 1.
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J. Gen. Virol. 83:2075-2083(2002).
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Best Local Similarity 80.0°
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Matches 4; Conservative
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RESULT 49 Q8JV16

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RESULT 50 Q8JV18 ID Q8JV10 AC Q8JV10 DT 01-OC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-9436951; PubMed=8081985; Ball-Goodrich L.J., Johnson E.; Ball-Goodrich L.J., Johnson E.; Ball-Goodrich L.J., Johnson E.; Wolecular characterization of a newly recognized mouse parvovirus."; J. Virol. 68:6476-6486(1994). EMBL; U12469; AAA61405.1; -. GO; GO:0019017; Civirion; IEA. GO; GO:0019017; Piviral genome replication; IEA. Interpro; IPR001257; Parvo NS1. Fam: Pr01057; Parvo NS1; I. Nonstructural protein. SEQUENCE 672 AA; 76112 NW; 31C6365276727363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse parvovirus 1.
Viruses; 8sDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=35340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=86115415; PubMed=3502703;
Astell C.R., Gardiner B.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mio
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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Pred. No. 5.5e+02;
1; Mismatches 0; Indels
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80.0%; Pred. No. 5.8e+02;
ive 1; Mismatches 0; Indels
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SEQUENCE 721 AA; 81862 MW; 9FD29C327C7F4BBF CRC64;
                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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J. Virol. 570:656-669(1986).
EMBL; M12032; AAA69566.1; -.
PIR; A23008; UYPVIM.
GO; GO:0019012; C:virion; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
InterPro; IPR001257; Parvo NSI.
PEam; PF01057; Parvo NSI; I.
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                                                                                                                                                                                                      Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26, Nonstructural protein 1.
                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Query Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 80.0
                                                                                                     PRELIMINARY;
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378 CHAIC 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                        Name=NS1;
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                                                                                                     Q83429
Q83429;
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     RESULT 52
1083429
AC 08342
DT 01-N0
DT 01-N0
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OC 
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08436
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DT 01-NO
DR 00; G
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Dutative far-red impaired response protein.
Name=P0472F10.13-1;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MVM;
MEDLINE=86115415; PubMed=3502703;
Astell C.R., Gardiner B.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83143341; PubMed=6298737;
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                              Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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80.0%; Pred. No. 5.8e+02;
ive 1; Mismatches 0; Indels
                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
721 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                815 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 11:999-1018(1983)
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prototype strain.";
J. Virol. 57:656-669(1986)
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Best Local Similarity 80..
Best Local 4; Conservative
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                               Nonstructural protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10794;
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Change S. From N. T. C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chow Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chen Y.-L., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chen Y.-L., Chang C.-H., Chung C.-I., Han S.-Y., Haido S.-H.,
Haido J.-N., Hau C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Li Y.-P., Shaw J.-P.,
Nu H.-P., Shaw J.-P.,
Co, Go. Go. Go. Start Character acid binding; IEA.
Co, Go. 1PR001876; F.nucleic acid binding; IEA.
InterPro; IPR001878; Znf_CHC.
R InterPro; IPR001878; Znf_ENZ.
R InterPro; IPR00554; Znf_ENZ.
R InterPro; IPR00181; Inf_SNIM.
R Fam; PF04434; SNIM; 1.
R Fam; PF04098; zf.CCHC; 1.
R SWART; SM00575; Znf_PMZ; 1.
R Hypothetical protein.
SQ SEQUENCE 1092 AA; 122243 MW; 8A9BS0FD758COEA5 CRC64;
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Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones;
Buthida, Buthoidea, Buthidae, Mesobuthus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 33; DB 2; Length 109
80.0%; Pred. No. 8.5e+02;
ative 1; Mismatches 0; Indels
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InterPro; IPR012061; Scorpion toxinL.
RNNTS; PR000285; SCORPWTOXINL.
ProDom; PD000908; Scorpion toxinL; 1.
3D-structure; Ionic channel inhibitor; Neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 AA.
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Beet Local Similarity 80.vv.
Bectonal 4; Conservative
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Matches 4; Conservative
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805 CHAIC 809
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                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                             NCBI_TaxID=39947;
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P60277;
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          SO WE WELL TO BE WELL 
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ORFNames-OSJNBa0068N06.23;

ORFyza sativa (japonica cultivar-group).

Eukaryota, Viridiplantae; Streptrophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017100, AAPS4042.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.1%; Score 33; DB 2; Length 929; 80.0%; Pred. No. 7.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%; Score 33; DB 2; Length 815; 80.0%; Pred. No. 6.5e+02; ive 1; Mismatches 0; Indels
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GO; GO:0003676; F:nucleic acid binding; IEA.

InterPro; IPR001878; Znf CCHC.

Pfam; PF00098; zf-CCHC; J.

SMART; SM00343; ZnF C2HC; J.

SEQUENCE 929 AA; 104564 MW; FEBFAD5D49F09300 CRC64;
          (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                             InterPro; IPR004330; FARI.
InterPro; IPR004330; FARI.
InterPro; IPR003654; Znf_PMZ.
InterPro; IPR007527; Znf_SWIM.
Pfam; PF03101; FARI; 1.
Pfam; PF04434; SWIM; 1.
SMART; SW00575; Znf_PMZ; 1.
PROSITE; PSS0811; MRXY; 1.
SRQUENCE 815 AA; 92895 MW; 003FD2ED7784E1C4 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBa0088M05.7.
Name=OSJNBa0088M05.7;
Oryza sativa (japonica cultivar-group).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                   EMBL; AP004877; BAD28228.1; -. GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 300:1566-1569(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 80.0
Matches 4, Conservative
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352 CHAIC 356
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(07XDU)
(07XDU)
AC 07XDU
DT 01-OC
DT 01-MA
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DE PLUAL
GN ONY 28
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0614D3
1D 0614D
AC 0614D
DT 05-JU
DT 05-JU
DE HYPOT
GN Name-
OS Oryza
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Gaps

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ö Gaps ö Score 31; DB 1; Length 64; Pred. No. 1.4e+02; 1; Mismatches 0; Indels 7041 MW; 06A852E2F5B0B934 CRC64;

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Q8D488; Q8D488

RESULT 59
080488
AC 080489
AC 080489
DT 01-MAD

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Horia K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Mondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Obaton N., Osazoki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Asakai D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
"Normalization and subtraction of cap-trapper-selected cDNAs to
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRANT-GSTBL/GJ TISSUE-Lung;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                              01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
MUB musculus 13 days embryo lung CDNA, RIKEN full-length enriched
library, clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETRAINS—CSTBL/64): TISSUB=Lung;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Natawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunal T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiiwagi K.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka M., Ohara B., Matahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                          Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                     PRT;
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                     PRELIMINARY;
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                                                                                                                                                                                       sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
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                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBL_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria, Gammaproteobacteria, Vibrionales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%; Score 31; DB 2; Length 108; 80.0%; Pred. No. 2.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016813; AAO08302.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 108 AA; 11846 MW; FB92F8EA3E170EAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genbur Acc. - Embl. 5406345; BAC96284.1; -. Complete proteome; Hypothetical protein. Complete proteome; Hypothetical protein. eranmence 116 AA; 12693 MW; 19B1D5E12C9C108B CRC64;
                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein VVA0258.
                                                                                                                                           108 AA
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                                                                                                                                                                                         Created)
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                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein. OrderedLocusNames=VV21423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=VVA0258;
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Matches 4; Conservative
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Matches 4; Conservative
                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=CMCP6;
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22 CHALC 26
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57 CHSVC 61
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RESULT 60
COMPREZ
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RESULT 61

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RESULT 62

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIR=AV19 / DSM 6334 / JCM 9639;

WEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;

Slegarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.I., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

TT and monophly of archeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL; AE010380; AAM02116.1; -:

RSP; PO0193; P:electron transporter activity; IEA.

GO; GO:0005489; P:electron transporter activity; IEA.

GO; GO:000518; P:electron transport; IEA.

RO; GO:0005189; P:electron transport; IEA.

PRINTS; PR00133; 4FE45FRDOXIN.

PRINTS; PR00196; TYTOCHROME_C; UNKNOWN I.

PROSITE; PS00190; CYTOCHROME_C; UNKNOWN I.

PROSITE; PS00190; CYTOCHROME_C; IITON: Bullfur; Metal-binding.

SEQUENCE 139 AA; 15190 MW; CE929F07722287FE CRC64;
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STRAIN=11pan, Davis, and 33spa;

STRAIN=11pan, Davis, and 33spa;

STRAIN=21053521; Pubmed=11773418;

Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;

"Identification of glycoprotein gpTRL10 as a structural component of human vycomegalovirus";

J. Virol. 76:1450-1460(2002).

EMBL; AF432081; AAL27466.1;

EMBL; AF432084; AAL27466.1;

EMBL; AF432087; AAL27466.1;

EMBL; AF432087; AAL27469.1;

Pfam; PF06084; Cytomega TRL10; 1.

SRQUENCE 168 AA; 18762 MW; B18FA2748C12F431 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 139;
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80.0%; Pred. No. 3.5e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
TRL10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.2%; Score 31; DB 2; I 80.0%; Pred. No. 2.9e+02; rative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 168 AA
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57 CHAMC 61
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05-JUL-2004 (
05-JUL-2004 (
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Q91019;
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Q6SX91
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KEUINE-21874850; PubMed=11878922; DOI=10.1006/viro.2001.1245;

KEUINE-21874850; PubMed=11878922; DOI=10.1006/viro.2001.1245;

KEDLINE-21874850; PubMed=11878922; DOI=10.1006/viro.2001.1245;

Long Q.X., Wang X.Z., Chan S.M.;

Long Q.X., Wang X.Z., Chan S.M.;

If "Sequence analysis of the complete genome of an iridovirus isolated from the tiger frog.";

Virology 29:185-197(2002)

C. -- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTWP.

C. -- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTWP.

C. -- SIMLARITY: Belongs to the thymidylate synthase family.

REBL: AFSB9451; ALJ7812.1; -.

REBL: AFSB9451; P.T. ALJ7812.1; -.

REBL: AFSB9451; P.T. ALJ7812.1; -.

REBL: AFSB9451; P.T. ALJ7812.1; -.

ROJ: GO:000479; P.T. ALJ7812.1; -.

ROJ: GO:000479; P.T. ALJ7812.1; EA.

GOJ: GO:000479; P.T. ALJ7812.1; EA.

GOJ: GO:000521; P.T. ALJ7812.1; EA.

ROJ: GO:000539; Thymidylate synth.

Rean, P. PODON; P. THYMDSNTHASE.

REINTS: PRO0108; THYMDSNTHASE.

REINTS: RODON; PRO0108; THYMDSNTHASE.

REINTS: RODON; REINTS: PRO0108; THYMDSNTHASE.

REINTS: RODON; THYMDSNTHASE.

REINTS: RODON; REINTS: RODON; THYMDSNTHASE.

REINTS: RODON; THYMDSNTHASE.

REINTS: RODON; REINTS: RODON; THYMDSNTHASE.

REINTS: RODON; THYMDSNTHASE.
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Methanopyrus kandleri.
Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                              Gape
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NCBI_TaxID=160691;
                                                                                               91.2%; Score 31; DB 2; Length 118; 80.0%; Pred. No. 2.5e+02; ive 1; Mismatches 0; Indels
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                                al protein.
118 AA; 12409 MW; 9DE6A7E88C8575BC CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thymidylate synthage-like protein.
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           EMBL; AK084985; BAC39329.1; -.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                               Query Match
Best Local Similarity 80.0°
....hag 4; Conservative
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Matches 4; Conservative
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NCBI_TaxID=2320;
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01-JUN-2002 (
01-JUN-2002 (
                                Hypothetical
SEQUENCE 11
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RESULT 63 Q8TWX8

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Length 168;

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STRAIN=22alt;
MEDIATE=2163521; PubMed=11773418;
MEDIATE=2163521; PubMed=11773418;
Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
"Identification of glycoprotein gpTRL10 as a structural component of human cytomegalovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spaderna S., Blessing H., Bogner E., Britt W., Mach M.; "Identification of glycoprotein gpTRL10 as a structural component of
                                                                                                                                                                                                                                                                       STRAIN-Merlin;
PubMed=15105547; DOI=10.1099/vir.0.79888-0;
Pobmed=15105547; DOI=10.1099/vir.0.79888-0;
Adolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L., Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C., Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
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80.0%; Pred. No. 3.5e+02;
tive 1; Mismatches 0; Indels
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80.0%; Pred. No. 3.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          "Genetic content of wild-type human cytomegalovirus.";
J. Gen. Virol. 85:1301-1312(2004).
BMBL; AF432089; AAL27471.1; -.
EMBL; AF446899; AAR315641.; -.
Ffam; PP066084; Cytomega TRL10; 1.
SEQUENCE 170 AA; 18974 MW; 7C850ABBEF36E61C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human cytomegalovirus.";
J. Virol. 76:1450-1460(2002).
EMBL, AF412085; AAL27467:1; -.
SEGUENCE 170 AA; 19031 MW; 7B7827917BFCB80C CRC64;
Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                    Virol. 76:1450-1460(2002).
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                         NCBI_TaxID=10359;
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59 CHAMC 63
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Q914P9
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PubMed=15105547; DOI=10.1099/vir.0.79888-0;
Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
                                                                                                                                                                         Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L., Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C., Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W., Davison A.J.;

"Genetic content of wild-type human cytomegalovirus.";

"Genetic content of wild-type human cytomegalovirus.";

"Genetic content of wild-type human cytomegalovirus.";

EMBL, AN46861, ARA31252.1;

InterPro; IPRO5084; Cytomega TRL10.

Pfam; PF06084; Cytomega TRL10.

Pfam; PF06084; Cytomega TRL10.

Pfam; BF06084; Cytomega TRL10.
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"Genelic content of wild-type human cytomegalovirus.";
J. Gen. Virol. 85:1301-1312(2004).
EMBL; AY446860; AAR31235.1;
InterPro; IPR009284; Cytomega TRL10.
Pfam; PF060084; Cytomega TRL10;
Pfam; PF060084; Cytomega TRJ0, 1.
SEQUENCE 168 AA; 18763 NW; CODA9297670DAD86 CRC64;
                    Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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Viruses; dsDNA viruses, no RNA stage, Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                           PubMed=15105547; DOI=10.1099/vir.0.79888-0;
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01-DEC-2001 (TEMBLEEL 19,
05-JUL-2004 (TEMBLEEL 27,
TRL10.
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Best Local Similarity 80.vv,
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57 CHAMC 61
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57 CHAMC 61
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RESULT 67 Q914P6 ID Q914P AC Q914P DT 01-DE DT 05-JU DE TRL10

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Curr. Top. Microbiol. Immunol. 154:125-169(1990).

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Spaderna S., Bleesing H., Bogner E., Britt W., Mach M.;
"Identification of glycoprotein gpTRL10 as a structural component
human cytomegalovirus.";
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N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
2C2E8AD869419B86 CRC64;
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Pfam; PF06084; Cytomega_TRL10; 1.
Glycoprotein; Hypothetical protein; Signal; Transmembrane.
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                                                                                                                                                                                                         J. Virol. 76:1450-1460(2002).
EMBL; AF432083; AAL27465.1; -.
Pfam; PF06084; Cytomega_TRL10; 1.
SEQUENCE 170 AA; 19032 MW; 7876C7917BFCB80C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
Hypochetical protein IRL10 precursor (TRL10).
Human cytomegalovirus (strain AD169).
Viruses; deDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                    Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 80.vv,
Best Local 4; Conservative
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                                                                                              NCBI_TaxID=10359;
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"Identification of glycoprotein gpTRL10 as a structural component of human cytomegalovirus.";
J. Virol. 76:1450-1460(2002).
PEBL; AF412088; AALZ-470.1;
PEAM; PF06084; Cytomega TRL10; 1.
SEQUENCE 171 AA; 19035 MM; 2C206AD869419B86 CRC64;
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Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
Horsnell T., Hutchison III C.A., Kouzarides T., Martignetti J.A.,
Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
#Analysis of the protein coding content of human cytomegalovirus
strain AD169.";
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Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Chee M.S.,
Hutchinson III C.A., Kouzarides T., Martignetti J.A., Preddie E.,
Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
"The DNA sequence of the human cytomegalovirus genome.";
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80.0%; Pred. No. 3.5e+02;
tive 1; Mismatches 0; Indels
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Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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Betaherpesvirinae; Cytomegalovirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
02-NUL-2004 (TrEMBLrel. 27, Last annotation update)
HCMVTRL10 = IRL10 protein.
Name=HCMVTRL10 = IRL10;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Query Match 91.2%; Score 31; DB 1; I Best Local Similarity 80.0%; Pred. No. 3.5e+02; Matches 4; Conservative 1; Mismatches 0;
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Viruses; dsDNA viruses, no
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CHAMC 64
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MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;

MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;

Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,

Alcendor D.J., McGeoch D.J., Hayward G.S.;

"The human cytomegalovirus genome revisited: comparison with the chimpanze cytomegalovirus genome.";

J. Gen. Virol. 84:17-28(2003).

J. Gen. Virol. 84:17-28(2003).

EMBL/GenBank/DDBJ third party annotation (TPA) entry.

RELICEPTO: IPR009284; Cytomega TRL10.

REPENDLY PR006984; Cytomega TRL10.

REPENDLY PR006984; Cytomega TRL10; 1.

SEQUENCE 171 AA; 19034 MW; 2C2E8ADR69419B86 CRC64;
                                                                                                                                                                              PubMed=15105547; DOI=10.1099/vir.0.79888-0; Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L., Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C., Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
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                                                                                                                                                                                                                                                                Davison A.J.;
"Generic content of wild-type human cytomegalovirus.";
J. Gen. Vic. B5:1301-1312(2004).

EMBL, AX446859; AAR31217.1;
-InterPro; IPR009284; Cytomega TRL10.
Pfam; PF06084; Cytomega TRL10; 1.

SEQUENCE 171 AA; 19006 MW; CDAA427AE376BE25 CRC64;
                       Human cytomegalovirus.
Viruses; daDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Matches 4; Conservative
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PubMed=15105547; DOI=10.1099/vir.0.79888-0;
Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L., Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C., Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W., Davison A.J.;
Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W., Garifiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
"Genetic content of wild-type human cytomegalovirus.";
J. Gen. Virol. 85:1301-1312(2004).
EMBL; AX446862; AAR31268.1;
Interpro; IPR00284; Cytomega_TRL10.
                                                                                                                                                                                                 Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J., Alcendor D.J., McGeoch D.J., Hayward G.S.;
"The human cytomegalovirus genome revisited: comparison with the chimpanzee cytomegalovirus genome.";
J. Gen. Virol. 84.17-28(2003).

EMBL; X17403; CAA15458.1;
EMBL; X17403; CAA15458.1;
PIR; S09759; S09759.
PIR; S09759; S09759.
PIR; S09759; S09759.
PIR; S09769; SYtomega_TRL10.
Peam; PF06084; Cytomega_TRL10.
Peam; PF06084; Cytomega_TRL10.
Peam; PF06084; Cytomega_TRL10.
Peam; PF06084; Cytomega_TRL10.
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                                                                                                                                                                                    MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;
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80.0%; Pred. No. 3.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              91.2%; Score 31; DB 2; Length 171;
80.0%; Pred. No. 3.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                  Submitted (DEC-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF06084; Cytomega TRL10; 1.
SEQUENCE 171 AA; 19016 MW; 23F9220850767E96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last sequence update)
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Geskce,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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hes 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytomegalovirus.
DNA Seq. 2:1-12(1991)
                  [3]
SEQUENCE FROM N.A.
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CHAMC 64
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                                                            STRAIN=AD169;
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RESULT 73 Q6SX75

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Best Loc Matches

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RESULT 74
Q6SXC6
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A bukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Indotani K., Ishii Y., Itoh M., Kagawa I., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
A katoh H., Kawai J., Kojima Y., Myazaki A., Murata M., Nakamura M.,
A kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A saito R., Saitoh H., Sakai K., Sakazume N., Osazaki Y.,
A saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Osano H.,
A saito R., Saitoh H., Sakai V., Shiraki T., Sogabe Y., Tagami M.,
A Tomaru A., Toya T., Yagumishi A., Muramata W., Hayashizaki Y.,
A Tomaru A., Toya T., Yagumishi A., Muramata W., Hayashizaki Y.,
A Tomaru A., Toya T., Yagumishi A., Muramata W., Hayashizaki Y.,
Bubmitted (Apr. 2002) to the EMBL/GenBank/DDBJ databases.
C. -- CATALYITC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NOD; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                          STRAIN=NOD; TISSUE=Thymus; MEDLINE-927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Mildhefficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
              Mus musculus 2 days neonate thymus thymic cells CDNA, RIKEN full-
length enriched library, clone:E430021G10 product:thymidylate
synthase, full insert sequence. (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NOD; TISSUB=Thymus; MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500; RIKEN PANTOM CONSOCTIUM; RIKEN PANTOM CONSOCTIUM; Nature 409:685-690(2001).
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-!- PATHWAY: Deoxyribonucleotide biosynthesis.
-!- SIMILARITY: Belongs to the thymidylate synthase family.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60,770 full-length cDNAB.";
Nature 420:563-573(2002).
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STRAIN=NOD; TISSUE=Thymus;
The PANTOM Consortium,
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STRAIN-NOD; ITSSUE-Thymus;
The FANTOM CONSOLL-thum.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
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01-OCT-2003 (TrEMBLEE]: 25, Last annotation update)
01-OCT-2003 (TrEMBLEE]: 25, Last annotation update)
10-OCT-2003 (TrEMBLEE]: 25, Last annotation update)
10-OCT-2003 (TrEMBLEE]: 25, Last annotation update)
10-OCT-2003 (TrEMBLEE): 10-OCT-2003 (TrEMBLEE)
10-OCT-2003 (TrEMBLEE): 10-OCT-2003 (
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 4.5e+02;
1; Mismatches 0; Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
EMBL; AK088606; BAC40450.1; -.
HSSP; P04818; 11HW3.
NGD; MGI:98878; TYME,
CG; GO:0008168; F:methyltransferase activity; IEA.
CG; GO:00016749; F:thymidylate synthase activity; IEA.
CG; GO:0006749; F:thymidylate synthase activity; IEA.
CG; GO:0006213; P:transferase activity; IEA.
CG; GO:0000215; P:nucleotide blosynthesis; IEA.
TIGEPIED; IPRO0308; THYMIdylat, synth.
PFANTS; PRO0308; THYMDSNITHASE.
                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001180; Thymidylat synth; 1.
PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
Methyltransferase; Nucleotide biosynthesis; Transferase.
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Best Local Similarity ' 80.0%;
Matches 4; Conservative 1
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STRAIN=E8V-1;
A Delarcque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W.;
A Delarcque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W.;
L Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

BR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

BR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

BR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

BR GO; GO:0004842; P:ubiquitin-protein ligase activity; IEA.

BR GO; GO:0004842; P:ubiquitination; IEA.

BR GO; GO:0016567; P:protein ubiquitination; IEA.

BR InterPro; IPR001841; Znf fing.

BR InterPro; IPR001841; Znf fing.

BR PROSITE; PS00190; CYTOCHEOME C; UNKNOWN 1.

BR PROSITE; PS50089; ZF RING 2; 1.
Hisatomi H., Tanemura H., Iizuka T., Katsumata K., Nagao K.,
Sumida H., Udagawa H., Hikiji K.;
"Differential alternative splicing expressions of thymidylate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
                                                                                                     Cancer Lett. 193:127-131(2003).
-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP dihydrofolate + dTMP.
-!- PATHWAY: Deoxyribonucleotide biosynthesis.
-!- PATHWAY: Deoxyribonucleotide biosynthesis.
-!- SIMILARITY: Belongs to the thymidylate synthase family.
-!- SIMILARITY: BAB83676.1; -.
                                                                                                                                                                                                                                                                  HSSP; P04818; IHVY.

GO; GO:0008166; F:nethyltransferase activity; IEA.

GO; GO:0004799; F:thymidylate sctivity; IEA.

GO; GO:0016740; F:thymidylate sctivity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:thymidylate sctivity; IEA.

GO; GO:0016916; P:norleotide biosynthesis; IEA.

PEam; PF00303; THYMIDSNTHASE.

PRODUM; PD001180; THYMIDYLATE SYNTH, 1.

PROSTE; PS00091; THYMIDYLATE SYNTHASE; 1.

PROSTECT 230 AA; 26140 MW; D09F8316ASO4A02A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 31; DB 2; Length 230; 80.0%; Pred. No. 4.7e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UTN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 80.vv,
4; Conservative
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112 CHALC 116
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Q9FYL9;
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Matches
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Q8QNP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9FYL9
ID Q9
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SEQUENCE FROM N.A.

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,

Saito H., Saitoh H., Sakai C., Sakai M., Sakazume N., Sano H.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

C. I- CATALYTIC ACTIVITY: 5,10-methyleneterrahydrofolate + dUMP =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE=22592598; PubMed=12706868; DOI=10.1016/S0304-3835(03)00005-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                        STRAIN=NOD; TISSUB-Thymus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateunnoto H., Sakaguchi S., Ikegami T., Kabhiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Natsuura S., Kawai J., Riksi integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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- LINGUAGREE + GINE.

- I STRILARITY: Decoxytbonucleotide biosynthesis.

- I SIMILARITY: Belongs to the thymidylate synthase family. BENDL, AK088134; BAC40165.1; -.

R KSSP; P45352; IRTS.

R MGD; MGI:98878; TYME.

GO; GO:00004799; F:thymidylate synthase activity; IEA.

GO; GO:00004799; F:thymidylate synthase activity; IEA.

R GO; GO:0000531; P:dTMP biosynthesis; IEA.

R GO; GO:0001655; P:nucleotide biosynthesis; IEA.

R GO; GO:0001655; P:nucleotide biosynthesis; IEA.

R Falm; PRO0033; Thymidylat synth.

R PRIMTS; PRO0108; THYMNONTHASE.

R PRODOM; PRO001180; THYMNONTHASE.

R PRODOM; PRO001180; THYMIDYLATE SYNTHASE; 1.

R PRODOM; PRO001180; THYMIDYLATE SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 222;
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80.0%; Pred. No. 4.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 AA; 25209 MW; 3E8DBDAF742DCC01 CRC64;
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Last annotation update)
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09WYK4
AC Q8WYK
DD 01-MA-
DT 01-MA-
DT 01-MA-
DT 01-MA-
DT 01-CA-

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Gaps

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Gaps

Created)

(TrEMBLrel. 16,

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Matches
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                                                                                                                                                                                          Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Wukharsky N., Nayyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Tottumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,

Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,

Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,

Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,

Ecker J.R., Theologis A.,

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, ACOCOLO3, AAF97956.1; --
                                                          Arabidopsis thallana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haag B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.2%; Score 31; DB 2; Length 251;
80.0%; Pred. No. 5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:00004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IERO1841; Znf_ring.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29487 MW; FCAA26695D467218 CRC64;
               01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
P21J9.10 (Hypothetical protein At1g24440).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00518; ZF RING 1; UNKNOWN 1. PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22088475; Pubmed=12093376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY085533; AAM62757.1; -. BT000927; AAN41327.1; -.
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251 AA; 2
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                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation.";
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                                                                                                                                                                                                                                                                                                Ecker J.R.;
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburnar M., Henderson S.N., Sutton G.G., Wortunan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazei R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril W.R., Basu A., An H.J., Andrews-Pfenankoch C., Baldwin D., Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                           MEDLINE=22829867; PubMed=12949112;
DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.B., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                            Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete Genome requence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
FIRE, AE017177; AAQ66714.1; -..
TIGR; PG1703; DEATH_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.2%; Score 31; DB 2; Length 261
80.0%; Pred. No. 5.2e+02;
ive 1; Mismatches 0; IndelB
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MazG family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 AA
  261 AA
                                              Created)
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                                                                                                                                                                                                             Porphyromonadaceae; Porphyromonas.
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TIGRFAMs; TIGR00444; mazG; 1.
                                              (TrEMBLrel. 26,
                                                                                                                                        OrderedLocusNames=PG1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR011551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 261 AA;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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CHALC 93
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                                                                                                                                                                                                                                        NCBI_TaxID=837;
                                              01-MAR-2004
                                                                                                                                                                                                                                                                                                          STRAIN=W83
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Q7MU57
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Gaps

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Local Similarity 80.0

Best Loc Matches

171 CHAMC 175

1 CHAVC 5

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Length 272;

91.2%; Score 31; DB 2; I 80.0%; Pred. No. 5.4e+02;

272 AA; 30172 MW; 4CCBAC7C10321322 CRC64;

SEQUENCE Query Match

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gurtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gaprielian A.E., Garg N.S., Gelbart W.M., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Harris M.,
Antis N.L., Harvey D., Heanan T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Martei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
RA Malson D.R., Nolson K., Nixon K., Nusskern D.R., Nelson D.L.,
RA Rolanc C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.Y., Wassarman D.A., Weinsecok G.M., Weissenbach J.,
RA Rhe R.F., Zavveri Y., Worley E., Wang G., Zhong E.,
RA Rhe R.F., Zaveri Y., Saunders E., Wang A.H., Wang X.,
RA Mang Z.Y., Wassarman D.A., Weinsecok G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.W., Rubin G.M., Venter J.C.;
RA Rhe Shue S.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sanith H.O.,
RA Zheng X.H., Shong F.W., Rubin G.M., Venter J.C.;
R. Reinber R.M., Rober E.W., Rubin G.M., Venter J.C.;
R. Rift G. Shan M., Rubin G.M., Venter J.C.;
R. Reinber R.W., Rubin G.M., Venter J.C.;
R. Reinber R.W., Rubin G.M., Venter J.C.;
R. Reinber R.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminher J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22456069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Submitted (MAR-2004) to the El
EMB., AB003730; AAF55759.2; -
FlyBase; FBgn0038791; CG4342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
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                    Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Lett. 193:127-131 (2003).
-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP dihydrofolate + dTMP.
-!- PATHWAY: Deoxyribomolectide biosynthesis.
-!- PATHWAY: Deoxyribomolectide biosynthesis.
-!- SIMILARITY: BABB03677.1; -.
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Pred. No. 5.6e+02;
1; Mismatches 0; Indels
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GO; GO:0004799; F:thymidylate synthase activity; IEA.
GO; GO:0004799; F:thymidylate synthase activity; IEA.
GO; GO:0006231; P:tTANSferase activity; IEA.
GO; GO:00005135; P:THYM biosynthesis; IEA.
FAM: PF00303; Thymidylat synt; 1.
PRINTS; PR00108; THYMDSNTHASE.
Propom; PD01180; Thymidylat synth; 1.
Methyltransferase; Nucleotide biosynthesis; Transferase.
SEQUENCE 279 AA; 31758 MM; 10B3A53DE10AB763 CRC64;
                  0; Indels
                                                                                                                                                                                                                   (TrEMBLrel. 20, Last sequence update) (TrEMBLrel. 25, Last annotation update)
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01-APR-1988 (Rel. 07, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Thymidylate synthase (EC 2.1.1.45) (TSase).
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                  1; Mismatches
                                                                                                                                                                                                  Created)
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MEDLINE=88174353; Pubmed=3444407;
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80.0%;
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Local Similarity 80.0
nes 4; Conservative
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nes 4, Conservative
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                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLre Thymidylate synthase.
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                                                                                  55 CHALC 59
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                                                  1 CHAVC 5
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P07607;
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Maley F
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                           MEDLINE=89128436; PubMed=2915925;
Deng T., LI Y., Johnson L.F.;
Deng T., LI Y., Johnson L.F.;
Deng T., LI Y., Johnson L.F.;
Thymidylate synthase gene expression is stimulated by some (but not all) introns.";
Nucleic Acids Res. 17:645-658 (1989).
-!- CATALYITC ACTIVITY: 5.10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.
-!- CATALYITC ACTIVITY: 5.10-methylenetetrahydrofolate + dUMP = -1. SUBUNIT: Homodimer.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to the thymidylate synthase family.
Perryman S.M., Rossana C., Deng T., Vanin E.F., Johnson L.F.; "Sequence of a cDNA for mouse thymidylate synthase reveals striking similarity with the prokaryotic enzyme."; Mol. Biol. Evol. 3:313-321(1986).
                                                                                              Deng T., Li D., Jenh C.-H., Johnson L.F.;
"Structure of the gene for mouse thymidylate synthase. Locations of
introns and multiple transcriptional start sites.";
J. Biol. Chem. 261:16000-16005 (1986).
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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InterPro; IPR000398; Thymidylat_synth.
Pfam; PF00303; Thymidylat_synt; 1.
PRINTS; PR001018; Thymidylat_synt; 1.
PRODOM; P0001180; Thymidylat_synth; 1.
PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
PROSITE: 189 BY SIMILATIC;
PROGUENCE 307 AA; 34958 MW; E4930618C487FD5E CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Thymidylate synthase (EC 2.1.1.45) (TS) (TSase)
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EMBL; JOSCHT; AAA40444.1; JOINED.
EMBL; M13347; AAA40444.1; JOINED.
EMBL; M13349; AAA40444.1; JOINED.
EMBL; M13349; AAA40444.1; JOINED.
EMBL; M13350; AAA40444.1; JOINED.
EMBL; M13351; AAA40444.1; JOINED.
EMBL; M13351; AAA40444.1; JOINED.
EMBL; K14489; CAA32651.1; -.
HSSP; P45352; IRTS.
                                                                     SEQUENCE FROM N.A.
MEDLINE=87057259; PubMed=3782103;
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Best Local Similarity
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P45352;
01-NOV-1995 (
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NORD TATABLE STATEMENTS ROGERIAS Sciurognathii Muridae; Murinae; Rattue.

NORD TATABLES STATEMENTS ROGERIAS RESIDENCY OF STATEMENTS REAL RESIDENCY REAL MATERIALS REAL MATERIAL REAL MATERIA
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SEQUENCE FROM N.A.

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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akimura T., Fukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,

Muramatsu M., Hayshizaki Y.,

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

C. -I- CATALYITC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =

dihydrofolate + dTMP.
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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R GO; GO:0008168; F:methyltransferase activity; IEA.

R GO; GO:0008168; F:methyltransferase activity; IEA.

R GO; GO:0006739; F:thymidylate synthase activity; IEA.

R GO; GO:0006231; P:dTyM biosynthesis; IEA.

R GO; GO:0009165; P:nuclectide biosynthesis; IEA.

R InterPro; IPR000398; Tymidylat_synth.

R Pfam; PF00303; Thymidylat_synth.

R Pfam; PF00303; Thymidylat_synth.

R Pfam; PF00309; THYMIDYLATE.

R PROSITE; PS00091; THYMIDYLATE_SYNTHASE; I.

R PROSITE; PS00091; THYMIDYLATE_SYNTHASE; I.

Methyltransferase; Nucleotide biosynthesis; Transferase.

SEQUENCE 307 AA; 34989 MW; E4930618C52CETEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- PATEWAY: Deoxyribonucleotide biosynthesis.
-1- SIMILARITY: Belongs to the thymidylate synthase family.
EMBL; AK011435; BAB27620.1; -.
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Last annotation update)
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Pred. No. 6.1e+02;
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80.0%;
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STRANT=C57BL/G17 IISSUE=Whole body;
MEDLINE=C57BL/G17 IISSUE=Whole body;
MEDLINE=C57BL/G17 IISSUE=Whole body;
MEDLINE=C97BL/G17 IISSUE=Whole body;
MEDLINE=C97BL/G17 IISSUE=Whole bold=101101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10 days embryo whole body CDNA, RIKEN full-length
enriched library, clone:2610017G21 product:thymidylate synthase, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/67; TISSUE=Whole body; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Melid-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 1; Length 307;
Pred. No. 6.1e+02;
1; Mismatches 0; Indels
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                       35017 MW; 159F564D347B2B52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AA
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STRAIN=CS7BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%;
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213
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253
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272
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287
307 AA;
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Best Local Similarity
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Districhench L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton B., Ketteman M., Madan A.M., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Xrzzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;

""" "Generation and initial malysis of more than 15,000 full-length human
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Strausberg R.; Subil/GenBank/DDBJ databases. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. -!- CALIVIIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP dihydrofolate + dTMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MG19876 TYME.

MGD; MG19876 TYME.

GO; GO:0008168; F:methyltransferase activity; IEA.

GO; GO:0006799; F:thymidylate synthase activity; IEA.

GO; GO:0006231; P:transferase activity; IEA.

GO; GO:0006231; P:dTMP biosynthesis; IEA.

GO; GO:0009165; P:nuclectide biosynthesis; IEA.

FEAM; PRO0305; THYMIDYLATE.

PEAM; PRO0108; THYMIDYLATE.

PRODOM; PD001180; THYMIDYLATE.

PROSITE; PS00091; THYMIDYLATE.

PROSITE; PS00091; THYMIDYLATE.

MOEHYLTENSFERSE; Nuclectide biosynthesis; Transferase.

SEQUENCE 307 AA; 34930 MW; 76F797162468FD9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- PATÄWAY: Deoxyribonucleotide biosynthesis.
-1- SIMILIMARITY: Belongs to the thymidylate synthase family.
EMBL; BCO20139; AAH20139.1; -.
HSSP; P45152; IRTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 31; DB 2; Length 307; 80.0%; Pred. No. 6.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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STRAIN-CZECH II, TISSUE-Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
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Best Local Similarity 80.0°
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GH05248p (Fragment).
ORFNames=CG4342;
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Q8MQS5;
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Q8MQS5
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TISSUE-Bone marrow, and Placenta;

XX TISSUE-Bone marrow, and Placenta;

XX TISSUE-23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Altscharko L., Marushina K., Parmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marushina K., Parmer A.A., Rubin G.M., Hong L.,

XX Diapleton M., Soares M.B., Ponshyuki S., Carninci P., Prange C.,

XX Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

XX Altalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

XX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

XX Butterfield X.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

XX Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

XX Generation and initial analysis of more than 15,000 full-length human
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Shichijo S., Itoh K.;
"Identification of immuno-peptidmics that recognized by tumor-reactive
CTL generated from TIL of colon cancer patients.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=91056070; Pubmed=2243092;
Kaneda S., Nalbantoglu J., Takeishi K., Shimizu K., Gotoh O., Seno T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ayusawa D.;
"Structural and functional analysis of the human thymidylate synthase
                                                                                                                                                                                                                                                                                                     Gapa
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01-WAR-1989 (Rel. 10, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
25-JAN-2005 (Rel. 46, Last annotation update)
Thymidylate synthase (EC 2.1.1.45) (TS) (TSase) (OK/SW-cl.29).
Name=TYMS; Synonyms=TS;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-85215997; Pubmed=2987839;
Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T
"Nucleotide sequence of a functional cDNA for human thymidylate
                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                        Length 310;
                                                                                                                                                                                                                                                                                                 0; Indels
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY128415; AAM75008.1; --
FlyBase; FBgn0038791; CG4342.
                                                                                                                   NOW TER 1 1 SEQUENCE 310 AA; 34213 MW; 7641F9761512F5CC CRC64;
                                                                                                                                                                                                                    91.2%; Score 31; DB 2; I
80.0%; Pred. No. 6.1e+02;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 AA
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                                                                                                                                                                                                                                                              Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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P04818;
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                                                                                                                                                                                                                               Query Match
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PDB; 1JUJ; X-ray; A/B/C/D=1-312.
Genew; HGNC:12441; TYMS.
                        H-InvDB; HIX0017793;
                                  Reactome; P04818; -.
MIM; 188350; -.
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SEQUENCE OF 1-67 FROM N.A.

MEDLINE=90110051; PubMed=2512645;
Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;
"Human thymidylate synthase gene: isolation of phage clones which cover a functionally active gene and structural analysis of the region Jubstream from the translation initiation codon.";
J. Biochem. 106:575-583 (1989).
                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE=96110704; PubMed=8845352;
Schiffer C.A., Clifton I.J., Davisson V.J., Santi D.V., Stroud R.M.;
"Crystal structure of human thymidylate synthase: a structural
mechanism for guiding substrates into the active site.";
Biochemistry 34:16279-16287(1995).
                                                                                                                              SEQUENCE OF 1-24.
MEDLINE-85261174; PubMed=3839505;
Shimizu K., Ayusawa D., Takeishi K., Seno T.;
"Putification and NH2-terminal amino acid sequence of human thymidylate synthase in an overproducing transformant of mouse FM3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

MEDLINE-21216721; PubMed=11278511; DOI=10.1074/jbc.M009493200;
Phan J., Steadman D.J., Koli S., Ding W.C., Minor W., Dunlap R.B.,
Berger S.H., Lebioda L.J.

"Structure of human thymidylate synthase suggests advantages of
emencherapy with noncompetitive inhibitors.";
J. Biol. Chem. 276:14177(2001).

-! CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
dihydrofolate + dTMP.

-! PATHWAY: Deoxyribonucleotide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=21229106; PubMed=11329255; DOI=10.1021/bi0024131;
MEDLINE=21229106; PubMed=11329255; DOI=10.1021/bi0024131;
Phan J., Koli S., Minor W., Dunlap R.B., Berger S.H., Lebioda L.;
"Human thymidylate synthase is in the closed conformation when complexed with dump and raltitrexed, an antifolate drug.";
Biochemistry 40:1897-1902(2001).
                                                                                                                                                                                                                                                 Davisson V.J., Sirawaraporn W., Santi D.V.; "Expression of human thymidylate synthase in Escherichia coli."; J. Biol. Chem. 264:9145-9148(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the thymidylate synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1HVY; X-ray; A/B/C/D=25-312.

1HW3; X-ray; A=1-312.

1HW4; X-ray; A=1-312.

1HZW; X-ray; A/B=23-312.

1100; X-ray; A/B=23-312.

1JU6; X-ray; A/B-23-312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AB062290; BAB93473.1; -.
L; BC002567; AAH02567.1; -.
L; BC013919; AAH13919.1; -.
L; D00517; BAA00404.1; -.
; A23047; XXHUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X02308; CAA26178.1; -. EMBL; D00596; BAA00472.1; -.
                                                                                                                                                                                                      Biochem. 97:845-850(1985)
                                                                                                                                                                                                                             SEQUENCE OF 1-9.
                                                                                                                                                                                                                                           PubMed=2656695;
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EMBL;
EMBL;
EMBL;
PDB;
PDB;
11
PDB;
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GO: 0000157; P:deoxyribonucleoside monophosphate biosynthesis; TAS.
GO: 0006139; P:nucleobase, nucleoside, nucleotide and nucl. .; TAS.
InterPro: 1PR000309; THYMIdylat synth.
ProDom: PF00108; THYMIDYLATE SYNTHASE; 1.
PROSITE; PR00108; THYMIDYLATE SYNTHASE; 1.
PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
3D-structure; Direct protein sequencing; Methyltransferase;
Nucleotide biosynthesis; Transferase.
INIT MET 0 0
ACT SITE 194 194
TURN
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Pred. No. 6.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35584 MW; A66P0E6D1973AB41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
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                                                                                                    312 AA;
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Best Local Similarity
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194 CHALC 198
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8

RESULT

Created) Last sequence update) Last annotation update)

224,25

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MEDINE-STATE FACTOR AND AND ADDRESS AND AD
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopteryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopteryoti, Neopteryoti, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
                                                                                      Tyms protein.
ORFNames=zgc:56465;
Brachydanio rerio (Zebrafish) (Danio rerio)
                  01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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  Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A phopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
Stapleton M., Soares M.B., Bonaldo M.F., Carahnaf L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohlyuki S., Carahnaf P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial malysis of more than 15,000 full-length human
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                                                     05-JJJ-2004 (TrEMBLrel. 27, Created)
05-JJJ-2004 (TrEMBLrel. 27, Last sequence update)
05-JJJL-2004 (TrEMBLrel. 27, Last annotation update)
2gc:56465 protein.
Name=zgc:56465; ORRNames=zgc:77659;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Caniata: Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii: Teleostei: Ostariophysi: Cypriniformes;
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                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (GAN-2004) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP dihydrofolate + dTMP.
--- PATHWAY: Decoxyribonuclectide biosynthesis.
--- SIMILARITY: Belongs to the thymidylate synthase family.
EMBL, BC065845; AAH65845.1; --
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Pred. No. 6.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00108; THYMDSNTHASE.
Prodom; PD001180; Thymldylat synth; 1.
PROSITE; PS001091; THYMIDYLATE SYNTHASE; 1.
Methyltransferase; Nucleotide biosynthesis; Transferase.
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GO; GO:0008168; F:methyltransferase activity; IEA.
GO; GO:0004799; F:thymidylate synthase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016231; F:dTMP biosynthesis; IEA.
GO; GO:0009165; P:nucleotide biosynthesis; IEA.
InterPro; IPR000398; Thymidylat_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                         318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                           PRT;
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                         PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
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TISSUE=Whole;
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                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
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                           Q6P045
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HSSP;
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80.0%; Pred. No. 6.3e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                 FRINTS; PROCOSO THYMESNITASE.
PRODOM; PROCOSO THYMIGYLAL SYNTH, 1.
PROSTIE; PSOCOSI; THYMIGYLALE SYNTHASE; 1.
MCHYLLAGNGERSE; NUCLECTICE DIOSYNTHASE; 1.
SEQUENCE 319 AA; 36299, MW; ADFA451EIDDF891A CRC64;
and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                               319 AA
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nes 4; Conservative
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                                 SEQUENCE FROM N.A.
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319 AA.

PRT;

PRELIMINARY;

Q7ZUI7

RESULT 91 Q7ZUI7 ID Q7ZUI

200 CHALC 204

1 CHAVC 5

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91.2%; Score 31; DB 2; Length 373; 80.0%; Pred. No. 7.3e+02; ive 1; Mismatches 0; Indels
   Waterston R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                 Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       WormBase; WBGene00020843; T27A3.7.
WormPep; T27A3.7; CE14229.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
InterPro; IPR00245; CytC heme BS.
InterPro; IPR002219; DAG FE-bind.
InterPro; IPR011011; FXVE_PHD_ZNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00109; C1; 1. _ _ _ BROSTE; PS 001190; CYTOCHROME_C; UNKNOWN_1.

Hypothetical protein. 42560 WW; FSDDFEFC9FCF29B9 CRC64; SEQUENCE
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PIR; T25920; T25920.
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Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
Matches 4; Conserva
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SEQUENCE 380 AA;
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                                                                                    SEQUENCE FROM N.A.
                                                                                                                STRAIN-Bristol N2;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Q8EED1
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2097 (TrEMBLrel. 26, Last annotation update)
010-MAR-2004 (TrEMBLrel. 26, Last annotation update)
14-MAP-2014 protein T27A3.7.

Name-T27A3.7; ORFNames=T27A3.7;
Caenorhabditis elegans.
Ebukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                      Gill R.L. Jr., Warren J.T. Jr.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 31; DB 2; Length 319; 80.0%; Pred. No. 6.3e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000398; Thymidylat_synth.
Pfam; PF000303; Thymidylat_synt; 1.
PRINTS; PR00108; THYMIGNTHASE.
ProDom; PD001180; THYMIGYLATE_synth; 1.
PROSTIE; PS00091; THYMIDYLATE_SYNTHASE; 1.
Methyltransferase; Nucleotide biosynthesis; Transferase.
SEQUENCE 319 AA; 36313 WM; E08B155B09DE1E84 CRC64;
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Murray J., Wohldmann P.;
"The sequence of C. elegans cosmid T27A3.";
Submitted (PEB-1997) to the EMBL/GenBank/DDBJ databases.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                           dihydrofolate + dTMP.
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                                                                                       Thymidylate synthase.
ORFNames=zgc:56465;
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201 CHALC 205
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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P91501
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      SOW WHEN THE PROPERTY OF THE P
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Gaps

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ö MEDLINE=22297686, PubMed=12368813, DOI=10.1038/nbt749;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.,
Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
Utterboack T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
Venter J.C., Nealson K.H., Fraser C.M.; Gaps Shewanella oneidensis. Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella. .; 0 91.2%; Score 31; DB 2; Length 380; 80.0%; Pred. No. 7.4e+02; tive 1; Mismatches 0; Indels 380 AA; 42539 MW; 562E0C3E60B5CF0F CRC64; 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SO2451.
OrderedLocusNames=SO2451; 380 AA Nat. Biotechnol. 20:1118-1123(2002). EMBL; AE015686; AAN55485.1; -. 1 CHAVC 5 ò Length 391;

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Query Match 91.2%; Score 31; DB 2; Length 391 Best Local Similarity 80.0%; Pred. No. 7.6e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                           Name=alg2-prov;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative.
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                                                                                                                                                                                                RESULT 97
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotia; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
NCBI_TaxID=305;
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STRAIN=ATCC 10895;
Gates K., Dietrich F.S., Brachat S., Voegeli S.E., Lerch A.,
Philippsen P., Gaffney T.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE016818; AAS52810.1; -.
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80.0%; Pred. No. 7.5e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21681879; Pubmed=11823852; DOI=10.1038/415497a;
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                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PUTATIVE TRANSERASE PROTEIN (EC 2.--).
Name-RS02347; OrderedLocusNames-RSD1013;
Ralstonia solanacearum (Pseudomonas solanacearum).
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Last annotation update)
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InterPro; IPR011257; DNA glycsylse.
InterPro; IPR003265; Endo 3c.
Pfam; PF00730; HhH-GPD; 1.
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CHSVC 25
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Strausberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Blant N.K.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Blant N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Garvinci P., Prange C.,

Raba S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Scheir human

M. Mones S.J., Marra M.A.,

Pand mouse CNNA secriances "...
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Gapa
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Klein S., Gerhard D.S.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071444; AMH77444.1; -..
GO, GO.00958; P:biosynthesis; IEA.
InterPro; IPR001296; Glyco_trans_1.
Pfam; PP00554; Glycos trans[1, 1.
Pfam; PP00554; Glycos trans[1, 1].
                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                        404 AA.
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Best Local Similarity 80.00,
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                                                                                                                                                 142 CHALC 146
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01-MAR-2004 (
01-MAR-2004 (
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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BNA Res. 9:189-197(2002).
EMBL; AP005958; BAC51568-1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000271; P:polysaccharide biosynthesis; IEA.
InterPro; IPR002797; Polysacc_synt.
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                                                                                                                                                                                                                                                                                             Neurospora crassa.
Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ALG70004; CAD21256.1;
GO; GO:0005622; C:intracellular; IEA.
GO; GO:000540; C:ribosome; IEA.
GO; GO:0003135; F:structural constituent of ribosome; IEA.
GO; GO:0006412; F:spructural constituent of ribosome; IEA.
REm; PRO1016; Ribosomal L27; 1.
PRINTS; PRO0063; Ribosomal L27; 1.
REDSOM; DD00314; Ribosomal L27; 1.
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Raddyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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80.0%; Pred. No. 8.6e+02;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Related to 60s ribosomal protein L2 (Mitochondrial)
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Last annotation update)
                                                                                                                      447 AA
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                                                                                                                         PRELIMINARY;
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18 CHSVC 22
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  73 CHALC 77
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                                                                                                                                                                                                                                                                    Name=5E6.150
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Q89GP2;
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Matches
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Anophales gambiae arr. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                              91.2%; Score 31; DB 2; Length 481;
80.0%; Pred. No. 9.2e+02;
iive 1; Mismatches 0; Indels
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80.0%; Pred. No. 9.6e+02;
tive 1; Mismatches 0; Indels
                                                 52048 MW; CAD37FB12B1B34D8 CRC64;
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SEQUENCE 502 AA; 55977 MW; 89AC334BCE3B2E8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Job time : 178 secs
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Pfam; PF01943; Polysacc_synt; 1.
Complete proteome.
SEQUENCE 481 AA; 52048 MW; C.
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                   Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                     389 CHALC 393
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Sequence 93, Appl
Sequence 91, Appl
Sequence 81, Appl
Sequence 82, Appl
Sequence 81, Appl
Sequence 82, Appl
Sequence 101, Appl
Sequence 111, Appl
Sequence 113, Appl
Sequence 13, Appl
Sequence 11, Appl
     Sequence 10, Sequence 296, Sequence 20, Sequence 81, A Sequence 81, A Sequence 88, A Sequence 89, A Sequence 90, A Sequence 10, Sequenc
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16 US-10-632-678-10
16 US-10-759-79-296
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18 US-10-759-79-296
18 US-09-769-145-81
18 US-09-769-145-89
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Sequence 296, App
Sequence 10, Appl
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                                                                                                                                                                                                         July 27, 2005, 00:01:11; Search time 157 Seconds (without alignments) 12.388 Million cell updates/sec
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Sequence 10,
Sequence 10,
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                                            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-105-928-296
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US-10-05-008-96
US-10-058-028-10
US-10-359-546-10
US-10-369-226-22
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Maximum Match 100%
Listing first 100 summaries
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and is derived by analysis of
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Post-processing:

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Title: Perfect 6

Sequence:

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Total number

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Searched:

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Gaps
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| SOFTWARE: Patentin Ver. 2.0
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 10
| LENGTH: 5
| TYPE: PRT
| ORGANISM: Artificial Sequence
| FEATURE: OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
| OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
| OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
| OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
| OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-769-145-10
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APPLICANT GOUR, Barbara J.
APPLICANT Blaschuk, Orest W.
APPLICANT Ali, Anmar
APPLICANT Ali, Anmar
APPLICANT Michael Stephanie
APPLICANT Michael Stephanie
APPLICANT Mang, Stephanie
APPLICANT Wang, Shoameng
APPLICANT Wang, Shoameng
APPLICANT WINGWINDON PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086,413C1
CURRENT APPLICATION NUMBER: US/09/769,145
CURRENT APPLICATION NUMBER: US 09/491,078
PRIOR PILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
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Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
CELL ADHESION
                PEATURE:
OTHER INFORMATION: DESCription of Artificial Sequence: ProcOTHER INFORMATION: Synthesis and Cyclization based on Human OTHER INFORMATION: N-Cadherin
                                                                                                                                                                 Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
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100.0%; Pred. No. 1.6e+06;
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100.0%; Pred. No. 1.6e+06;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED IP LAW GROUP PLLC
                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09769145
Patent No. US20020168761A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10006982 Publication No. US20020151475A1 GENERAL INFORMATION:
                                                                                        FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-296
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 ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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Sequence 190876,
Sequence 762, App
Sequence 201825,
Sequence 118366,
Sequence 183087,
                                                  Sequence 18655,
Sequence 146, App
Sequence 150, App
Sequence 35523, A
Sequence 174571,
Sequence 211467,
Sequence 211467,
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                                     Sequence 197899,
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Sequence 296, Application US/09234395

Sequence 296, Application US/09234395

Sequence 296, Application US/09234395

Sequence 296, Application US/09234395

Parent No. US20020123044A1

APPLICANT: Blaschuk, Orest W.

APPLICANT: Blaschuk, Orest W.

APPLICANT: Barbara J.

TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER

FILE REFERENCE: 100086-407C2

CURRENT APPLICATION NUMBER: 05/09/234,395

CURRENT FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 324

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 296

LENGTH: 5
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; Sequence 296, Application US/09305928
; Patent No. US20020146687A1
; GENERAL INFORMATION;
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; TILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305,928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SCOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 324
; SEQ ID NOS: 324
; SEQ ID NOS: 324
; SEQ IP NOS: 324
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c US-10-437-963-169219

c US-10-437-963-201319

C US-10-437-963-188559

c US-10-437-963-188559

c US-10-629-313-146

c US-10-629-313-146

c US-10-629-313-146

c US-10-63-313-1467

c US-10-437-953-114671

c US-10-437-953-114671

c US-10-424-599-163830

US-09-864-761-36833

US-10-424-599-190876

c US-10-425-15-201825

c US-10-425-15-201825

c US-10-425-15-201826

c US-10-424-959-183067
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ORGANISM: Artificial Sequence
FEATURE:
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                CHAVC 5
                CHAVC 5
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US-09-305-928-296
     FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as accetyl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or US-10-058-821-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-359-546-10

US-10-359-546-10

Sequence 10, Application US/10359546

Publication No. US20030224978A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara W.

TITLE OP INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS

FILE REFERENCE: 100086.401C15

CURRENT APPLICATION NUMBER: US/10/359,546

CURRENT FILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
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                                                                                                                            Sequence 10. Application US/10058821
Fublication No. US2030087811A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
TILE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
FILE REFERENCE: 100086. 401C12
CURRENT APPLICATION NUMBER: US/10/058,821
CURRENT FLING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
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100.0%; Score 34; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Publication No. US20030065136A1
GENERAL INFORMATION;
APPLICANT: Blaschuk, Orest W.
APPLICANT: Farockhi, Riaz
APPLICANT: Ali, Annar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401D1
CURRENT APPLICATION NUMBER: US/10/105,008
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-10-105-008-96
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     STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
                                                                                                                                                                  COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/006,982
FILING DATE: 04-Dec-2001
CLASSIFICATION: CUNKNOWN>
ATTORNEY AGENT INFORMATION:
NAME: Christiansen, William T.
RECISTRATION NUMBER: 44,614
RECISTRATION NUMBER: 100086.401C11
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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TOPOLOGY: «Itcular

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-006-982-8
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5 amino acida
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ORGANISM: Artificial Sequence
                               CITY: Seattle
STATE: Washington
COUNTRY: USA
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Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                       ZIP: 98104
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1 CHAVC 5
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/oz C-terminal modifications such as amide or
OTHER INFORMATION: ester group
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                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/369,226
FILING DATE: 13-Feb-2003
CLASSIFICATION: Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CLAISTEANTION:
NAME: CLAISTEANTION:
TELECOMMUNICATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406C3
TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
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100.0%; Pred. No. 1.6e+06;
Live 0; Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gour, Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
APPLICANT: Mi, Feng
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Wichaud, Stephanie Denise
APPLICANT: Wang, Shaomeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 10, Application US/10425557; Publication No. US20040006011A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5 amino acids
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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; Publication No. US2003023468A1
; GENERAL INFORMATION:
    APPLICANT: Blaschuk, Orest W.
    APPLICANT: Blaschuk, Orest W.
    Gour, Barbara J.
    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
    INTER OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seatile STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/369,226
FILING DATE: 13-Feb-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 34; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-10-369-226-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                           Sequence 22, Application US/10369226
Publication No. US20030236186A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104
COMPUTER READABLE FORM:
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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US-10-369-226-34
                                                                                                        RESULT 8
US-10-369-226-22
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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US-10-759-507-296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or CTHER INFORMATION: ester group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
                                                                                                                            APPLICANT: Blaschar J.
APPLICANT: Blaschar J.
APPLICANT: Blaschar J.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
APPLICANT: Ni, Feng
APPLICANT: Ni, Feng
APPLICANT: Wach, Zhigang
APPLICANT: Wach, Zengjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
CURRENT APPLICATION NUMBER US/10/412,701
CURRENT FILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 5
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                                                                    ; Sequence 10, Application US/10412701; Publication No. US20040058864A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Query Match

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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             sequence 200, Application us/10/2017)
publication No. US20040248219A1
GENERAL INPORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Byens, Stephen
ITILE OF INVENTION: Barbara J.
ITILE OF INVENTION: BATHODS FOR DIAGNOSING AND EVALUATING CANCER
FILE REFERENCE: 100006.407C12
CURRENT APPLICATION NUMBER: US/10/759,379
CURRENT APPLICATION NUMBER: 09/305,928
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-01.20
PRIOR FILING DATE: 1998-01.20
PRIOR FILING DATE: 1998-05-05
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Publication No. U320040248220A1

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Byers, Stephen
APPLICANT: Gour, Barbara J.
TILLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
FILE REPERENCE: 100086,407C11
CURRENT APPLICATION NUMBER: US/10/759,507
CURRENT APPLICATION NUMBER: 09/234,395
PRIOR FILING DATE: 1999-01-20
PRIOR PILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-05-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
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100.04; Score 34; DB 16;
Best Local Similarity 100.04; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 296, Application US/10759379 Publication No. US20040248219A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity
Matches 5; Conserv
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US-10-836-289-20
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                                                                                       GTHER INFORMATION: Description of Artificial Sequence: Product of
GTHER INFORMATION: Synthesis and Cyclization based on Human
GTHER INFORMATION: N-Cadherin
FEATURE:
GTHER INFORMATION: Cyclic Peptide
US-10-759-507-296
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Mi, Anmar
APPLICANT: Mi, Fengang
APPLICANT: Michaud, Stephanie
APPLICANT: Michaud, Stephanie
APPLICANT: Mang, Shohanie
APPLICANT: Mang, Shohanie
APPLICANT: Hu, Zengjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086, 413C1
CURRENT APPLICATION UNMERS: US/09/769, 145
CURRENT FILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20. Application US/10836289

Publication No. US20050004013A1
GENERAL INFORMATION:
APPLICANT THE SCRIPPS RESEARCH INSTITUTE
APPLICANT THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: Michael. I.
TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
TITLE OF INVENTION: METHODS
FILE REFERENCE: TSRI-987.1
CURRENT APPLICATION NUMBER: US/10/836,289
CURRENT APPLICATION NUMBER: 00/467,188
FRIOR PILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: APPLICATION NUMBER: OF SEQ ID NO 20
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: APPLICATION NUMBER: OF SEQ ID NO 20
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 20
CORNIEW NEWS APPLICATION NUMBER OF SEQ ID NO 20
SOFTWARE: PRICE FASISED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                           Length 5;
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100.0%; Pred. No. 1.6e+06;
cive 0; Mismatches 0;
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Patent No. US20020168761A1
GENERAL INFORMATION:
                                              ORGANISM: Artificial Sequence
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Best Local Similarity 100..
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Matches 5; Conservative
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TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
COGANISM: Artificial Sequence: Cyclic Peptide
FEATURE:
OTHER INFORMATION: Useription of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
OTHER INFORMATION:
                                                                                                                                                           TYPE: PRT

CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
US-09-769-145-81
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APPLICANT: Wang, Stoameng
APPLICANT: Hu, Zengjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100066.413C1
CURRENT FILIAG DATE: 2001-01-24
PRIOR APPLICATION NUMBER: US 09/491,078
PRIOR APPLICATION NUMBER: US 09/491,078
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 9; Length 6; 100.0%; Pred. No. 1.6e+06; ive 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 09/491,078
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 81
LENGTH: 6
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US-09-769-145-85
; Sequence 85, Application US/09769145
; Patent No. US20020168761A1
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie
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NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
Query Match
Best Local Similarity
Matches 5; Conserv
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US-09-769-145-90
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                                                                                                                         APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie
APPLICANT: Wang, Shoameng
APPLICANT: Wang, Shoameng
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
CURRENT APPLICATION NUMBER: US/09/769,145
CURRENT FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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PRIOR PELICATION NUMBER: US/09/769,145
PRIOR PELICATION DATE: 2001-01-24
PRIOR FILING DATE: 2000-01-24
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100.0%; Pred. No. 1.6e+06;
ttive 0; Mismatches 0;
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                                                                                                       Ni, Feng
Chen, Zhigang
Michaud, Stephanie
Wang, Shoameng
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                          : Gour, Barbara J.
: Blaschuk, Orest W.
: Ali, Anmar
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 88
LENGTH: 6
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       GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Ni, Feng
APPLICANT: Ni, Feng
APPLICANT: Ni, Cangiang
APPLICANT: Wang, Shoameng
APPLICANT: Wang, Shoameng
APPLICANT: Wang, Shoameng
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086,413C1
CURRENT FILING DATE: 2001-01-24
PRIOR PILLING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
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APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie
APPLICANT: Wang, Shoameng
APPLICANT: Hu, Zengilan
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.413C1
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                      Length
100.0%; Score 34; DB 9; L
100.0%; Pred. No. 1.6e+06;
M.comarches 0;
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CURRENT FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: US 09/491,078
PRIOR FILING DATE: 2000-01-24
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Sequence 89, Application US/09769145
Patent No. US20020168761A1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 89
LENGTH: 6
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Best Local Similarity 100.
Matches 5; Conservative
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SOFTWARE: Patentin Ver. 2.0
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                       SEQ ID NO 84
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APPLICANT: Farockhi, Riaz
APPLICANT: Ali, Anmar
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100096.401D1
CURRENT APPLICATION NUMBER: US/10/105,008
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 99
                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-03-769-145-90
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APPLICANT: Farockhi, Riaz
APPLICANT: Farockhi, Riaz
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401D1
CURRENT APPLICATION NUMBER: US/10/105,008
CURRENT APPLICATION NUMBER: 2002-03-22
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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Publication No. US20030065136A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
SEQ ID NO 90
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-105-008-10
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US-10-105-008-84
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; Sequence 87, Application US/2030065136A1
; GENERAL INPORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farockhi, Riaz
APPLICANT: Farockhi, Riaz
APPLICANT: Farockhi, Riaz
APPLICANT: Farockhi, Compounds AND METHODS FOR MODULATING CELL ADHESION
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; TILE OF INVENTION: COMPOUNDS
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 87
; TYPE: PRESTURE:
; ORGANISM: Artificial Sequence
; FEATURE:
; FEAT
TYPE: PRT

CRGANISM: Artificial Sequence
FRATURE:
CHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
US-10-105-008-84
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APPLICANT: Blaschuk, Darbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Farockhi, Riaz
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401D1
CURRENT APPLICATION UNDRES: US/10/105,008
CURRENT FILING DATE: 2002-03-22
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100.0%; Pred. No. 1.6e+06;
iive 0; Mismatches 0;
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Publication No. US20030065136A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-03-22
                     NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 92
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US-10-105-008-95
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Sequence 91, Application No. US20030065136A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Farcokhi, Riaz
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086, 401D1
CURRENT APPLICATION NUMBER: US/10/105,008
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 99
SOCTHARE: Patentin Ver. 2.0
SEQ ID NO 91
LENGTH: 6
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Publication No. US20030065136A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Farookhi, Riaz
APPLICANT: Farookhi, Riaz
TITLE OP INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401D1.
CURRENT APPLICATION NUMBER: US/10/105,008
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                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as accition or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
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tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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                   SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 88
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Sequence 93, Application US/10105008
Fublication No. US20030065136A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Farookhi, Riaz
APPLICANT: Ali, Anmax
TITLE REFERENCE: 100M90066.401D1
CURRENT APPLICATION NUMBER: US/10/105,008
CURRENT FILIAG DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030065136A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Farockhi, Riaz
APPLICANT: Farockhi, Riaz
APPLICANT: PAI, Anmar
APPLICANT: POINTON COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100066.401D1
                                                     PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
US-10-105-008-92
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TYPE: PRT ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: With Classical Cell Adhesion Recognition Sequence
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
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CTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
CTHER INFORMATION: ester group
US-10-425-557-84
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
                                                                                                APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Wang, Shaomeng
APPLICANT: Wang, Shaomeng
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086,401C16
CURRENT APPLICATION NUMBER: US/10/425,557
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEG ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Wang, Shaomeng
APPLICANT: Hu, Zenjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REPERENCE: 100066.4010.16
CURRENT APPLICATION NUMBER: US/10/425,557
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 85
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100.0%; Pred. No. 1.6e+06;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie Denise
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ORGANISM: Artificial Sequence
                          Blaschuk, Orest
Ali, Anmar
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Best Local Similarity 100.
Matches 5; Conservative
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
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APPLICANT: Michaud, Stephanie Denise
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Wang, Shaomeng
APPLICANT: Hu, Zenjian
TITLE OF INVENTION: PEPTICOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.401040
CURRENT APPLICATION NUMBER: US/10/425,557
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 81
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100.0%; Pred. No. 1.6e+06;
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CURRENT APPLICATION NUMBER: US/10/105,008
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 99
SSCTWARE: Patentin Ver. 2.0
SSCT ID NO 95
LENGTH: 6
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US-10-425-557-84
Sequence 84, Application US/1042557
Publication No. US20040006011A1
GENERAL INFORMATION:
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Annar
APPLICANT: Ni, Feng
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US-10-425-557-81
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal; OTHER INFORMATION: modification such as aceryl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or; OTHER INFORMATION: ester group
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ali, Anmar
APPLICANT: Ni, Peng
APPLICANT: Ni, Peng
APPLICANT: Michaud, Stephanie Denise
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SECTIONO 90
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APPLICANT: Michaud, Stephanie Denise
APPLICANT: Wang, Shoameng
APPLICANT: Hu, Zengjian
IITLE OP INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
                                                                                                                                                                                                                                ; Score 34; DB 15; Length 6; ; Pred. No. 1.6e+06; 0; Mismatches . 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90, Application US/10425557
Publication No. US20040006011A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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ORGANISM: Artificial Sequence
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Peng
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
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APPLICANT: Ali, Anmar
APPLICANT: Chen, Zhigang
APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Mand, Shaomeng
APPLICANT: Hu, Zenjan
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.401C16
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 906
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Gour, Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
APPLICANT: Chen, Zhiqang
APPLICANT: Wang, Shaomeng
APPLICANT: Wang, Shaomeng
APPLICANT: Hu, Zenjian

ITILE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFRENCE: 100066.401C16
CURRENT APPLICATION NUMBER: US/10/425,557
CURRENT APPLICATION NUMBER: US/10/425,557

CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 96

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 88
LENGTH: 6
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; Sequence 89, Application US/10425557
; Publication No. US20040006011A1
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ORGANISM: Artificial Sequence
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
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US20040058864A1
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                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or C-TER INFORMATION: ester group US-10-412-701-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Cyclic Peptide may comprise N-terminal CHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or US-10-412-701-84
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; Bedication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Mi. Anmar
; APPLICANT: Mi. Anmar
; APPLICANT: Mi. Peng
; APPLICANT: Mi. Peng
; APPLICANT: Mi. Peng
; APPLICANT: Mi. Peng
; APPLICANT: More and Stephanie Denise
; APPLICANT: More and Stephanie Denise
; APPLICANT: Wang, Shoameng
; NUMBER OF SEQ ID NOS PETTION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
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100.0%; Pred. No. 1.6e+06;
iive 0; Mismatches 0;
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FILE REFERENCE: 100086.413C2
CURRENT PEPLICATION NUMBER: US/10/412,701
CURRENT FILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 81
LENGTH: 6
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US-10-412-701-85
; Sequence 85, Application US/10412701
                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-412-701-84
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
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APPLICANT: Michaud, Stephanie Denise
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Manay Shoameng
APPLICANT: Hu, Zenglian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086, 413C2
CURRENT APPLICATION NUMBER: US/10/412,701
CURRENT FILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
                                                                                                                                                                                                                            TITE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION FILE REFERENCE: 100086.413C2
CURRENT APPLICATION NUMBER: US/10/412,701
CURRENT FILING DATE: 2.003-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 34; DB 15; Length 6; 100.0%; Pred. No. 1.6e+06; Live 0; Mismatches 0; Indels
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APPLICANT: GOUY, Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Annar
APPLICANT: Ni, Feng
APPLICANT: Chen, Zhigang
APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Wang, Shoameng
APPLICANT: Hu, Zengjian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 88, Application US/10412701
Publication No. US20040058864A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Blaschuk, Orest W.
APPLICANT: All, Anmar
APPLICANT: Ni, Feng
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TYPE: PRT ORGANISM: Artificial Sequence
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US-10-632-678-84
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CTHER INFORMATION: Cyclic Peptide may comprise N-terminal
CTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
COTHER INFORMATION: and/or C-terminal modifications such as amide or
COTHER INFORMATION: ester group
US-10-412-701-89
                                                                                                                                                                                                                                                              APPLICANT: Gour. Barbara J.
APPLICANT: Gour. Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Annar
APPLICANT: Ali, Annar
APPLICANT: Ni, Feng
APPLICANT: Chen, Zhigang
APPLICANT: Chen, Zhomenel
APPLICANT: Mchaud, Stephanie Denise
APPLICANT: Hu, Zengian
APPLICANT: Hu, Zengian
APPLICANT: Hu, Zengian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.413C2
CURRENT APPLICANTON NUMBER: US/10/412,701
CURRENT PILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 96
SOOTWARE: Patentin Ver. 2.0
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORMATION:
APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ali, Anmar
APPLICANT: Ali, Anmar
APPLICANT: Chen, Zhigang
APPLICANT: Mend, Shoameng
APPLICANT: Mend, Shoameng
APPLICANT: Hu, Zengjian
APPLICANT: Hu, Zengjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.413C2
CURRENT APPLICANTION NUMBER: US/10/412,701
CURRENT APPLICANTION NUMBER: 203-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 1.6e+06;
iive 0; Mismatches 0;
100.0%; Pred. No. 1.6e+06; ive 0; Mismatches 0;
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                                                                                                                                                                                                           Sequence 89, Application US/10412701 Publication No. US20040058864A1 GENERAL INFORMATION:
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Best Local Similarity 100.
                      5; Conservative
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Sequence 84, Application US/10632678
; Sequence 84 Application No. US20040106545A1
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Farookhi, Riaz
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPUNDS AND METHODS FOR MODULATING CELL ADHESION
; TITLE OF INVENTION: COMPOS. 101
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
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; Sequence 87, Application US/106545A1
; Dublication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farockhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SEQ ID NO 87
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; PEATURE: OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group; OTHER INFORMATION: ester group OTHER INFORMATION: ester group
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TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 5, Conservative
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NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 91
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Riaz
APPLICANT: Gour, Barbara J.
APPLICANT: Gour, Barbara J.
APPLICANT: Ali, Anmar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401C18
CURRENT PELLOATION NUMBER: US/10/632,678
CURRENT FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 6
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Sequence 91, Application US/10632678
Sequence 91, Application No. US20040106545A1
Sequence 91, DADICATION OX20040106545A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Ali, Annir
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REPERENCE: 100086.401C18
FILE REPERENCE: 100086.401C18
CURRENT APPLICATION NUMBER: US/10/632,678
CURRENT FILING DATE: 2003-08-01
                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl gr
OTHER INFORMATION: and/or C-terminal modifications such as amide
OTHER INFORMATION: ester group
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-632-678-88
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Sequence 92. Application US/10632678

| Sequence 92. Application US/20040106545A1
| Publication No. US20040106545A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. APPLICANT: Earookhi, Klaz APPLICANT: Farookhi, Klaz J. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICATION NUMBER: US/10/632,678
| CURRENT APPLICATION NUMBER: US/10/632,678
| CURRENT FILING DATE: 2003-08-01
| SOFTWARE: Patentin Ver: 2.0
| SEQ ID NO 92
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Sequence 93, Application US/10632678
Publication No. US20040106545A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Gover, Raiz
APPLICANT: Ali, Annar
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence FEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: and/or C-terminal modification such as acetyl or alkoxybenzyl group OTHER INFORMATION: and/or C-terminal modifications such as amide or OTHER INFORMATION: ester group
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ORGANISM: Artificial Sequence
PERATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-769-145-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or US-09-769-145-86
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; Sequence 87, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
    APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
APPLICANT: Ni, Feng
APPLICANT: Wang, Shoameng
; PRING PRILOTYION NUMBER: US 09/491,078
; PRIOR PILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOOTHWARE: Patentin Ver. 2.0
                    APPLICANT: Ni, Feng
APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie
APPLICANT: Michaud, Stephanie
APPLICANT: Michaud, Stephanie
APPLICANT: Wang, Shoameng
APPLICANT: Hu, Zengjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.413C1
CURRENT APPLICATION NUMBER: US/09/769,145
CURRENT FILING DATE: 2001-01-24
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN VET. 2.0
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
Ali, Anmar
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LENGTH: 7
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; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Bracchui, Riaz
; APPLICANT: Farookhi, Riaz
; APPLICANT: Farookhi, Riaz
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT PILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PATENTIN VET: 2.0
; SEQ ID NO 100
; SEQ ID NO 100
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
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                       CURRENT APPLICATION NUMBER: US/10/632,678
CURRENT FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 101
SEQTWARE: Patentin Ver. 2.0
SEQ ID NO 93
LENGTH: 6
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Patent No. US20020168761A1
GENERAL INFORMATION:
APPLICANT: GOUX, Barbara J.
APPLICANT: Blaschuk, Orest W.
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
  REFERENCE: 100086.401C18
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-632-678-100
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 5; Conservative
5; Conservative
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Sequence 90, Application US/10105008

Publication No. US20030065136A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Farockhi, Riaz

APPLICANT: Ali, Anmar

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

FILE REFERENCE: 100086.401D1

CURRENT FILING NAMBER: US/10/105,008

CURRENT FILING DATE: 2002-03-22

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 90

SEQ ID NO 90

LENGTH: 7
                                                                                                                                                                 Sequence 89, Application US/10105008

| Sequence 89, Application US/10105008
| Publication No. US2003006513611
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Ozest W. |
| APPLICANT: Barcockhi, Armar |
| APPLICANT: Rarockhi, Armar |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION |
| FILE REFERENCE: 1000086, 401D1 |
| CURRENT APPLICATION NUMBER: US/10/105,008 |
| CURRENT APPLICATION NUMBER: US/10/105,008 |
| CURRENT PILING DATE: 2002-03-22 |
| SOFTWARE: PATENTIN Ver. 2.0 |
| SEQID NO 89
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+06;
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APPLICANT: Chen, Zhigang
APPLICANT: Michaud, Stephanie Denise
APPLICANT: Mang, Shaomeng
APPLICANT: Wang, Shaomeng
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.401C16
CURRENT APPLICATION NUMBER: US,10/425,557
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 86
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APPLICANT: Michaud, Stephanie Denise
APPLICANT: Wang, Shaomeng
APPLICANT: Hu, Zenjian
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
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CURRENT APPLICATION NUMBER: US/10/425,557
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
LENGTH: 7
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; Sequence 86, Application US/10425557
; Publication No. US20040006011A1
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RESULT 58
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OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide CTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence; FEATURE: OTHER INFORMATION: Cyclic Peptide may comprise N-terminal OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group; OTHER INFORMATION: and/or C-terminal modifications such as amide or US-10-425-557-87
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OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
OTHER INFORMATION: ester group
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APPLICANT: Blaechuk, Orest W.
APPLICANT: Blaechuk, Orest W.
APPLICANT: Ali, Anmar
APPLICANT: Ni, Feng
APPLICANT: Ni, Feng
APPLICANT: Wand, Stephanie Denise
APPLICANT: Wand, Stephanie Denise
APPLICANT: Wang, Shoameng
APPLICANT: Wang, Shoameng
APPLICANT: Wang, Shoameng
APPLICANT: Hu, Zenglan
TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
FILE REFERENCE: 100086.413C2
CURRENT APPLICATION NUMBER: US/10/412,701
CURRENT APPLICANTON NUMBER: US/10/412,701
SOFTWARE: PALENTING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PALENTIN Ver. 2.0
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100.0%; Pred. No. 1.6e+06;
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Michaud, Stephanie Denise
Wang, Shoameng
Hu, Zengjian
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US-10-412-701-87
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Sequence 89, Application US/10632678
; Sequence 89, Application US/106345A1
; Bublication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; TITLE OF INVENTION NUMBER: US/10/632,678
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; SOPTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
LENGTH: 7
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COTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: and/or C-terminal modifications such as amide or
COTHER INFORMATION: ester group
US-10-632-678-89
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TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION FILE REFERENCE: 100086.413C2
CURRENT APPLICATION NUMBER: US/10/412,701
CURRENT FILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ 10 NO 87
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100.0%; Pred. No. 1.6e+06;
ative 0; Mismatches 0;
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; Sequence 90, Application US/10632678
; Publication No. US20040106545A1
; FIREMAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 5; Conservative
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US-10-632-678-101
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**APPLICANT: Gour, Barbara J.

APPLICANT: Farockhi, Riaz
APPLICANT: Farockhi, Riaz
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086,401C18
CURRENT APPLICATION NUMBER: US/10/632,678
CURRENT FILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 90
LENGTH: 7
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| Sequence 96. Application No. US20040106545A1 |
| Publication No. US20040106545A1 |
| GENERAL INFORMATION: |
| APPLICANT: Blascbuk, Orest W. |
| APPLICANT: Farookki, Riaz |
| APPLICANT: Ali, Anmar |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION |
| TITLE OF INVENTION: COMPOUNDS: US/10/632,678 |
| CURRENT APPLICATION NUMBER: US/10/632,678 |
| CURRENT APPLICATION NUMBER: US/10/632,678 |
| SOFTWARE: PAFENTING DAYS: 101 |
| SOFTWARE: PAFENTING VEY: 2.0 |
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100.0%; Pred. No. 1.6e+06;
iive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-632-678-96
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Sequence 101, Application US/106345A1

Bublication No. US20040106545A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: GOUX, Barbara J.

APPLICANT: Farcokhi, Riaz

APPLICANT: Ali, Anmar

TITLE OF INVENTION: COMPOUDS AND METHODS FOR MODULATING CELL ADHESION

FILE REFERENCE: 100086.401C18

CURRENT APPLICATION NUMBER: US/10/632,678

CURRENT FILING DATE: 2003-08-01

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 101
Publication No. US20040106545A1
GENERAL INFORMATION:
BAPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
APPLICANT: Farockhi, Riaz
APPLICANT: Ali, Anmar
ATTLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
FILE REFERENCE: 100086.401218
CURRENT APPLICATION NUMBER: US/10/632,678
CURRENT PILING DATE: 2003-08-01
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
PEATURE:
OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
OTHER INFORMATION: ester group
US-10-632-678-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence FEATURE:
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NAME/KEY: MOD_RES
LOCATION: (5)
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; OTHER INFORMATION: Where Xaa is beta,beta-dimethyl cysteine
US-10-632-678-101
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100..
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Best Local Similarity 100..
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Sequence 323830, Application US/10425115

Sequence 323810, Application US/2040214272A1

Sequence 323810, Application No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 323830
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: No. US20030228584Alel Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-045

CURRENT APPLICATION NUMBER: US/10/291,172

CURRENT FILING DATE: 2000-11-08

PRIOR PRING DATE: 2000-00-10

PRIOR PILING DATE: 2000-00-10

PRIOR APPLICATION NUMBER: 09/665,363

PRIOR PILING DATE: 2000-00-19

PRIOR PILING DATE: 2000-00-14

PRIOR PILING DATE: 2000-00-17

PRIOR PILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705

PRIOR PILING DATE: 2000-05-19

PRIOR PILING DATE: 2000-05-19
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100.0%; Pred. No. 3.1e+02;
ative 0; Mismatches 0;
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100.0%; Score 34; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: MRT4577_58402C.1.pep
US-10-425-115-323830
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Best Local Similarity 100.
Matches 5; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-630
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ORGANISM: Zea mays
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US-10-221-278-630
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; Sequence 133433, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION;
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Yahua
; APPLICANT: Boukharov, Andrey A.
APPLICANT: Bu, Wel
; APPLICANT: Bu, Wel
; APPLICANT: Li, Fing
; APPLICANT: Li, Fing
; TITLE OF INVENTION: Plant and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILE OF INVENTION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT SELING DATE: 2003-05-14
; WUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133433
                                                                                                                                                                                           Sequence 17220, Application US/10424599
| Sequence 17220, Application US/10424599
| Sequence 17220, Application US/20414599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongwei
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
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| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
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| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
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US-10-424-599-172220
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COTHER INFORMATION: Clone ID: PAT_MRT4530_35303C.1.pep
US-10-437-963-133433
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Glycine max
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30 CHAVC 34
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   3 CHAVC 7
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US-10-43/-303-13/415, Application US/10437963
; Sequence 137415, Application US/10437963
; Publication No. US2040123343A1
; GENERAL INPORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Shou, Yihua
; APPLICANT: Shou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brad
; APPLICANT: Brad
; APPLICANT: Brad
; APPLICANT: APPLICANTION: Plante and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 137415
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; Publication No. US20020119929A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Colin E.
; APPLICANT: Agoulnik, Alexander I.
; APPLICANT: Zhu, Qichao
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
; FILE REFERENCE: PO20664031/10024824
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT APPLICATION NUMBER: 60/245,872
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR PILING DATE: 200-11-03
; NUMBER OF SEQ ID NOS: 14
; SOFFWARE: Patentin version 3.1
; SEQ ID NO 8.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 34; DB 13; Length 380; 100.0%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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US-10-437-963-137415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-003-806-8
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5, Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 CHAVC 322
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Squence 198654, Application US/10437963

Squence 198654, Application US/10437963

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yogwei

APPLICANT: Cao, Yogwei

APPLICANT: Baubazuk, Brad

APPLICANT: Bring Paral Sand

APPLICANT: Bandbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5321)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 196854
                GENERAL INFORMATION:

JENERAL INFORMATION:

TITLE OF INVENTION: No. US20040034208Alel Nucleic Acids and Polypeptides

FILE REPERBERCE: 1272-045

FILE REPERBERCE: 2002-09-06

CURRENT FILING DATE: 2002-09-06

PRIOR PRILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-19

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 752
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100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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US-10-437-963-196854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 34; DB 16;
100.0%; Pred. No. 5.2e+02;
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US-10-003-806-8
; Sequence 8, Application US/10003806
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 CHAVC 117
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Sequence 191667, Application US/10425115
Sequence 191667, Application US/10425115
Publication No. US200402142721
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules Associated With
TITLE Acid Molecules Associated
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Actional M.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 315958
LENGTH: 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 33; DB 16; Length 76;
80.0%; Pred. No. 3.38+02;
/ative 1; Mismatches 0; Indels
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US-10-425-115-315958
                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
LENGTH: 537
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity 80.v.
A; Conservative
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; ORGANISM: Sus scrofa
US-10-047-542-74
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55 CHAIC 59
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US-10-425-115-191667
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US-10-437-963-197235

Sequence 197254, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Barbardk, Brad

APPLICANT: Barbardk, Brad

APPLICANT: Buckharcv, Andrey A.
APPLICANT: B
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION OF: 204966
SEQ ID NO 151715
LENGTH: 424
TYPE: ...
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Publication No. US2020168367A1
GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 34; DB 16; Length 513; 100.0%; Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_51834C.1.pep
US-10-437-963-151715
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US-10-437-963-197235
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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39 CHAVC 43
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US-10-047-542-74
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US-10-424-599-233727

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Sequence 233277

September 23229

September 23229

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September 23229

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

SEPTEMBER 2003-04-28

SEPTEMBER 23327

SEPTEMBER 23327

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.1%; Score 33; DB 15; Length 241; 80.0%; Pred. No. 8.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                    Length 110;
                                                                                                              97.1%; Score 33; DB 15; Length 11
80.0%; Pred. No. 4.4e+02;
tive 1; Mismatches 0; Indels
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_122038C.1.pep
US-10-424-599-167243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53080C.1.pep
US-10-424-599-233727
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US-10-424-599-276468
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Best Local Similarity 80.0%
                                                                                                                 Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: Glycine max
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104 CHAIC 108
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APPLICANT: Barbazuk, Brad ".

APPLICANT: Barbazuk, Brad ".

APPLICANT: Barbazuk, Brad ".

APPLICANT: Li, Ping ".

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement ".

FILE REFERENCE: 38-21(53221)8

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 159565

LENOTH: 102

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APPLICANT: La Rosa Thomas J
APPLICANT: About Xinua
APPLICANT: Zhou Yinua
APPLICANT: Zhou Yinua
APPLICANT: Zhou Yinua
APPLICANT: About Xinua
APPLICANT: APPLICANT: About Xinua
TITLE OF INVENITION: SOQ Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENITION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)223)B
FILE REFERENCE: 3003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 167243
LENGTH: 110
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                                                                                                                                               97.1%; Score 33; DB 16; Length 82; 80.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                         0; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_5892C.1.pep
US-10-437-963-159565
                              ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106382C.1.pep
US-10-425-115-191667
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LOCATION: (1)..(110)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15956, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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                                                                                                                    Ouery Match
Best Local Similarity 80.0.
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ORGANISM: Oryza Bativa
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ORGANISM: Glycine max
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50 CHAIC 54
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48 CHAIC 52
ORGANISM: Zea mays
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US-10-437-963-159565
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US-10-424-599-167243
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US-10-437-963-190970

Sequence 190970, Application US/10437963

Sequence 190970, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: Ex Rosa, Thomas J.

APPLICANT: APPLICANT: Cac, Yongwel

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brandard, Brand

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and UBes Thereof for Plant Improvement

FILE REFERENCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 190970
Sequence 71839, Application US/10425114

Sequence 71839, Application No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Schou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERBNCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 71839
LENGTH: 314
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97.1%; Score 33; DB 15; Length 314;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: UC-ZMFLB73165F09_FLI.pep
US-10-425-114-71839
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US-10-437-963-190972
; Sequence 190972, Application US/10437963
; Publication No. US20040123343A1
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Sequence 179189, Application US/10437963

Sequence 178189, Application US/10437963

Sebicarion No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Roses, Thomas J.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brabauk, Brad

APPLICANT: Brabauk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

SEQ ID NO 178188

SEQ ID NO 178189

LENGTH: 280
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80.0%; Pred. No. 9.3e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%; Score 33; DB 15; Length 243;
80.0%; Pred. No. 8.3e+02;
iive 1; Mismatches 0; Indels
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US-10-424-599-233725
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US-10-437-963-178188
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Glycine max
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106 CHAIC 110
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217 CHAIC 221
                              104 CHAIC 108
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RESULT 81

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Sequence 169219, Application US/10437963

Sequence 169219, Application US/10437963

Sequence 169219, Application No. US20040123343A1

Sequence 169219, Application No. US20040123343A1

Sequence 169219, Application No. US20040123343A1

Septicant: Line Comment Comm
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US-10-13/19-20-10113/
Sequence 201319, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brad
APPLICANT: Brad
APPLICANT: Brad
APPLICANT: Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 201319
LENGTH: 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.1%; Score 33; DB 16; Length 892; 80.0%; Pred. No. 2.3e+03; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%; Score 33; DB 16; Length 77'80.0%; Pred. No. 2.18+03; tive 1; Mismatches 0; Indels
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US-10-437-963-201319
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US-10-437-963-169219
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.1
Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 CHAIC 594
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US-10-437-963-201319
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APPLICANT: Rovalic, David K.
APPLICANT: Rovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122755
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5321)8

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

EDENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%; Score 33; DB 16; Length 426; 80.0%; Pred. No. 1.3e+03; ive 1; Mismatches 0; Indel8
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US-10-437-963-122755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT4530_87335C.1.pep
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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184 CHAIC 188
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US-10-437-963-122755
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RESULT 87 US-10-437-963-197899

RESULT 85

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Publication No. US20040176572A1
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Best Local Similarity 80.0
Matches 4; Conservative
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US-10-629-313-146
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9 CHALC 13
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; Sequence 188555, Application US/10437963
; Publication No. USZ004012334341
; GENERAL INFORMATION
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Buckharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPRENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; WUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 188555
; LENGTH: 946
| Sequence 197899, Application US/10437963
| Publication No. US20040123343A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Zhou, Yihua
| APPLICANT: Zhou, Yihua
| APPLICANT: Bubkharov, Andrey A.
| APPLICANT: Bubkharov, Andrey A.
| APPLICANT: Bubkharov, Andrey A.
| APPLICANT: Barbazuk, Brad
| APPLICANT: Li, Ping
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF EXPENTED OF THE PROPERTY OF THE PREFERENCE: 38-21 (53221)B
| CURRENT APPLICATION NUMBER: US/10/437,963
| SEQ ID NO 197899
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80.0%; Pred. No. 2.4e+03;
ive 1; Mismatches 0; Indels
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80.0%; Pred. No. 2.4e+03;
tive 1; Mismatches 0; Indels
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US-10-437-963-188555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_93612C.1.pep
US-10-437-963-197899
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US-10-629-313-146
; Sequence 146, Application US/10629313
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Matches 4, Conservative
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Matches 4; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682 CHAIC 686
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APPLICANT: Nation is Fremer to the control of the c
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CURRENT FLING DAYS

APPLICANT: La Rosa, Thomas J.
APPLICANT: Edou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174571
LENGTH: 49
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                             OTHER INFORMATION: MAP TO AP000512.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEARN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 9; Length 20;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 16; Length 49
Pred. No. 4.8e+02;
1; Mismatches 0; Indels
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US-10-437-963-174571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 174571, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Rank, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HARLE, David R.
APPLICANT: HARLE, David R.
APPLICANT: HARLE, David R.
APPLICANT: HARLE, David R.
ITILE OP INVERTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OP INVERTION: 2000-06-33
FRIOR PLILIANG DATE: 2001-06-33
FRIOR PLILIANG DATE: 2000-06-34
FRIOR PLILIANG DATE: 2000-06-34
FRIOR PLILIANG DATE: 2000-06-37
FRIOR PLILIANG DATE: 2000-06-37
FRIOR PLILIANG DATE: 2000-06-37
FRIOR PLILIANG DATE: 2000-06-37
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FRIOR PLILIANG DATE: 2001-06-37
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FRIOR PLILIANG DATE: 2001-01-37
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Pred. No. 2.2e+02;
1; Mismatches 0; Indels
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/106,056
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 150
LENGTH: 18
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Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 190876, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                           PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-21
PRIOR PILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
FEATURE:
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36 CHALC 40
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| Patent No. USZ00200048763A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G.
| APPLICANT: Rank, David R.
| APPLICANT: Hanzel, David R.
| APPLICANT: Chen, Wensheng
| TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR
| TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FOR TITLE OF INVENTION: HUWBER: US 00/0964, 761
| CURRENT APPLICATION NUMBER: US 00/180, 312
| PRIOR PILICATION NUMBER: US 00/180, 312
| PRIOR FILING DATE: 2000-02-04
| PRIOR FILING DATE: 2000-05-26
| PRIOR PILICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Exovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163830
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Pred. No. 4.9e+02;
1; Mismatches 0; Indels
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US-10-424-599-163830
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US-10-425-115-211467
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Pred. No. 5.2e+02;
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FILE REFERENCE: 38-21(55222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 211467
LENGTH: 51
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 80.0.
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Best Local Similarity 80.0
Matches 4; Conservative
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50 CHALC 54
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ORGANISM: Zea mays
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12 CHSVC 16
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Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: Oryza sativa
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75 CHAMC 79
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US-10-424-599-183087
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Cao, Yingwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 201825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 762, Application US/10291265

Sequence 762, Application US/10291265

Bublication No. US20030232054A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

TITLE OF ILING DATE: 2000-01-25

CURRENT FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR PELING DATE: 2000-01-25

PRIOR PELING DATE: 2000-07-17

PRIOR FILING DATE: 2000-07-17

PRIOR PELING DATE: 2000-09-15

PRIOR PELING DATE: 2000-09-15

PRIOR PELING DATE: 2000-09-15

PRIOR PELING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SEQ ID NO 762

TEMPORE 2000-09-15

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SEQ ID NO 762
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80.0%; Pred. No. 6.1e+02;
tive 1; Mismatches 0; Indels
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US-10-424-599-190876
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 190876
LENGTH: 67
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Best Local Similarity 80.0
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Matches 4; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-762
                                                                                                                                                           ORGANISM: Glycine max
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52 CHSVC 56
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81 CHSVC 85
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Sequence 118366; Application US/10437963
; Sequence 118366, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: 
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Sequence 183087, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 183087
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT4530_21685C.1.pep
US-10-437-963-118366
TYPE: PRT:
COCANISM: Zea mays
FEATURE:
NAME/KEY:
COCATION: (1)..(96)
COTHER INFORMATION: unsure at all Xaa locations
FEATURE:
COTHER INFORMATION: Clone ID: MRT4577_115648C.1.pep
US-10-425-115-201825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 16;
Pred. No. 8.1e+02;
1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.2%; Score 31; DB 16;
80.0%; Pred. No. 8.3e+02;
tive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.2%;
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136340C.1.pep
US-10-424-599-183087
```

Query Match 91.2%; Score 31; DB 15; Length 100; Best Local Similarity 80.0%; Pred. No. 8.48+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps

. 0

> 1 CHAVC 5 ||:|| 96 CHSVC 100

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